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OM protein - protein search, using sw model

Run on: January 28, 2006, 00:54:46 ; Search time 22 Seconds  
(without alignments)  
37.580 Million cell updates/sec

Title: US-09-018-194A-4

Perfect score: 57

Sequence: 1 CVGSNKGATC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5 COMB.pep.\*

2: /cgn2\_6/prodata/1/iaa/6 COMB.pep.\*

3: /cgn2\_6/prodata/1/iaa/H COMB.pep.\*

4: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*

5: /cgn2\_6/prodata/1/iaa/RE COMB.pep.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	2	US-09-163-095-4
2	57	100.0	10	2	US-09-866-898-4
3	57	100.0	10	2	US-09-632-748-4
4	43	75.4	123	2	US-09-771-161A-171
5	39	68.4	8	2	US-09-163-095-1
6	39	68.4	8	2	US-09-866-898-1
7	39	68.4	8	2	US-09-632-748-1
8	39	68.4	10	2	US-09-724-961-30
9	39	68.4	10	2	US-09-724-961-31
10	39	68.4	10	2	US-09-724-961-32
11	39	68.4	10	2	US-09-580-018-30
12	39	68.4	10	2	US-09-580-018-31
13	39	68.4	10	2	US-09-580-018-32
14	39	68.4	10	2	US-09-724-551-30
15	39	68.4	10	2	US-09-724-551-31
16	39	68.4	10	2	US-09-724-551-32
17	39	68.4	10	2	US-09-724-940-30
18	39	68.4	10	2	US-09-724-940-31
19	39	68.4	10	2	US-09-724-940-32
20	39	68.4	14	2	US-09-623-548A-958
21	39	68.4	14	2	US-09-623-548A-964
22	39	68.4	14	2	US-09-623-548A-991
23	39	68.4	14	2	US-09-657-276-958
24	39	68.4	14	2	US-09-657-276-964
25	39	68.4	14	2	US-09-657-276-991
26	39	68.4	24	2	US-09-623-548A-981
27	39	68.4	24	2	US-09-623-548A-1008
28	39	68.4	24	2	US-09-657-276-981
29	39	68.4	24	2	US-09-657-276-1008
30	39	68.4	26	1	US-08-304-585-7
31	39	68.4	33	1	US-08-609-090-4
32	39	68.4	34	1	US-08-475-579A-4
33	39	68.4	35	1	US-08-304-585-6
34	39	68.4	35	1	US-08-612-785B-16
35	39	68.4	35	1	US-08-612-785B-36
36	39	68.4	35	1	US-08-612-785B-39
37	39	68.4	35	1	US-08-612-785B-40
38	39	68.4	35	2	US-08-617-267C-15
39	39	68.4	35	2	US-09-623-548A-979
40	39	68.4	35	2	US-09-623-548A-1006
41	39	68.4	35	2	US-09-657-276-979
42	39	68.4	35	2	US-09-657-276-1006
43	39	68.4	36	1	US-08-609-090-6
44	39	68.4	38	1	US-08-302-808-1
45	39	68.4	38	1	US-07-737-371B-68
46	39	68.4	38	1	US-08-986-948-1
47	39	68.4	38	2	US-09-623-548A-975
48	39	68.4	38	2	US-09-623-548A-1002
49	39	68.4	38	2	US-09-657-276-975
50	39	68.4	38	2	US-09-657-276-1002
51	39	68.4	38	6	5262332-1
52	39	68.4	39	1	US-08-304-585-5
53	39	68.4	39	1	US-08-302-808-2
54	39	68.4	39	1	US-08-609-090-7
55	39	68.4	39	1	US-08-682-245A-1
56	39	68.4	39	1	US-08-986-948-2
57	39	68.4	40	1	US-07-744-767A-1
58	39	68.4	40	1	US-08-235-400-2
59	39	68.4	40	1	US-08-476-464A-2
60	39	68.4	40	1	US-08-304-585-1
61	39	68.4	40	1	US-08-304-585-8
62	39	68.4	40	1	US-08-302-808-3
63	39	68.4	40	1	US-08-433-734-1
64	39	68.4	40	1	US-08-609-090-8
65	39	68.4	40	1	US-07-737-371B-69
66	39	68.4	40	1	US-08-682-245A-2
67	39	68.4	40	1	US-08-986-948-3
68	39	68.4	40	1	US-08-461-216-1
69	39	68.4	40	2	US-08-959-148-1
70	39	68.4	40	2	US-09-242-724-22
71	39	68.4	40	2	US-08-723-661B-1
72	39	68.4	40	2	US-09-062-365-3
73	39	68.4	40	2	US-09-481-980A-5
74	39	68.4	40	2	US-09-133-866-1
75	39	68.4	40	2	US-09-988-842-3
76	39	68.4	40	2	US-10-455-218-1
77	39	68.4	40	2	US-10-151-614-1
78	39	68.4	40	2	US-09-623-548A-956
79	39	68.4	40	2	US-09-623-548A-962
80	39	68.4	40	2	US-09-623-548A-968
81	39	68.4	40	2	US-09-623-548A-978
82	39	68.4	40	2	US-09-623-548A-985
83	39	68.4	40	2	US-09-623-548A-995
84	39	68.4	40	2	US-09-623-548A-1005
85	39	68.4	40	2	US-09-657-276-956
86	39	68.4	40	2	US-09-657-276-962
87	39	68.4	40	2	US-09-657-276-968
88	39	68.4	40	2	US-09-657-276-978
89	39	68.4	40	2	US-09-657-276-989
90	39	68.4	40	2	US-09-657-276-995
91	39	68.4	40	2	US-09-657-276-1005
92	39	68.4	40	2	US-09-962-955D-36
93	39	68.4	40	4	PCT-US92-06700-1
94	39	68.4	41	1	US-07-819-361-1
95	39	68.4	41	1	US-08-302-808-4
96	39	68.4	41	1	US-08-682-245A-3
97	39	68.4	41	1	US-08-986-948-4
98	39	68.4	42	1	US-07-744-767A-2
99	39	68.4	42	1	US-08-179-574-1
100	39	68.4	42	1	US-08-271-162-5

## ALIGNMENTS

RESULT 1  
US-09-163-095-4  
; Sequence 4, Application US/09163095  
; Patent No. 6242416  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/163,095  
; CURRENT FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: PCT/US97/04966  
; EARLIER FILING DATE: 1997-03-28  
; EARLIER APPLICATION NUMBER: 08/625,765  
; EARLIER FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic peptide  
US-09-163-095-4

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVGSNKGGAIC 10  
Db 1 CVGSNKGGAIC 10

RESULT 2  
US-09-866-898-4  
; Sequence 4, Application US/09866898  
; Patent No. 6696303  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/866,898  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic peptide  
US-09-866-898-4

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVGSNKGGAIC 10

Db 1 CVGSNKGGAIC 10

RESULT 3  
US-09-632-748-4  
; Sequence 4, Application US/09632748  
; Patent No. 6867179  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND  
; TITLE OF INVENTION: COLORATION  
; FILE REFERENCE: 0054.1087-010  
; CURRENT APPLICATION NUMBER: US/09/632,748  
; CURRENT FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: PCT/US99/02362  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,194  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: US 08/793,683  
; PRIOR FILING DATE: 1995-08-30  
; PRIOR APPLICATION NUMBER: US 08/298,941  
; PRIOR FILING DATE: 1994-08-31  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic peptide  
US-09-632-748-4

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVGSNKGGAIC 10  
Db 1 CVGSNKGGAIC 10

RESULT 4  
US-09-771-161A-171  
; Sequence 171, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 171  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-171

Query Match 75.4%; Score 43; DB 2; Length 123;  
Best Local Similarity 60.0%; Pred. No. 5.7;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVGSNKGGAIC 10

Db 100 CRGNGRGAVC 109

## RESULT 5

US-09-163-095-1  
; Sequence 1, Application US/09163095  
; Patent No. 6242416  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/163,095  
; CURRENT FILING DATE: 1998-09-29  
; EARLIER APPLICATION NUMBER: PCT/US97/04966  
; EARLIER FILING DATE: 1997-03-28  
; EARLIER APPLICATION NUMBER: 08/625,765  
; EARLIER FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-163-095-1

Query Match 68.4%; Score 39; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 1 VGSNKGAI 8

## RESULT 6

US-09-866-898-1  
; Sequence 1, Application US/09866898  
; Patent No. 6696303  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/866,898  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 09/163,095  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-898-1

Query Match 68.4%; Score 39; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 1 VGSNKGAI 8

## RESULT 7

US-09-632-748-1  
; Sequence 1, Application US/09632748  
; Patent No. 6867179  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND  
; TITLE OF INVENTION: COLORATION  
; FILE REFERENCE: 0054-1087-010  
; CURRENT APPLICATION NUMBER: US/09/632,748  
; CURRENT FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: PCT/US99/02362  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,194  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: US 08/793,683  
; PRIOR FILING DATE: 1995-08-30  
; PRIOR APPLICATION NUMBER: US 08/298,941  
; PRIOR FILING DATE: 1994-08-31  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-632-748-1

Query Match 68.4%; Score 39; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.6e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 1 VGSNKGAI 8

## RESULT 8

US-09-724-961-30  
; Sequence 30, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-961-30

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

## RESULT 9

US-09-724-961-31  
; Sequence 31, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-961-31

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
| | | | |  
Db 2 VGSNKGAI 9

## RESULT 10

US-09-724-961-32  
; Sequence 32, Application US/09724961  
; Patent No. 6743427  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,961  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US 09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-961-32

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
| | | | |  
Db 1 VGSNKGAI 8

## RESULT 11

US-09-580-018-30  
; Sequence 30, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-30

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

## RESULT 12

US-09-580-018-31  
; Sequence 31, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-31

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 2 VGSNKGAI 9

RESULT 13  
US-09-580-018-32  
; Sequence 32, Application US/09580018  
; Patent No. 6761888  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/580,018  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-580-018-32

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 1 VGSNKGAI 8

RESULT 14  
US-09-724-551-30  
; Sequence 30, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-551-30

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 3 VGSNKGAI 10

RESULT 15  
US-09-724-551-31  
; Sequence 31, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-551-31

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 2 VGSNKGAI 9

RESULT 16  
US-09-724-551-32  
; Sequence 32, Application US/09724551  
; Patent No. 6787637  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/09/724,551

US-09-724-940-31  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-551-32

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 1 VGSNKGAI 8

RESULT 17  
US-09-724-940-30  
; Sequence 30, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-30

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 3 VGSNKGAI 10

RESULT 18

US-09-724-940-31  
; Sequence 31, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-31

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 2 VGSNKGAI 9

RESULT 19  
US-09-724-940-32  
; Sequence 32, Application US/09724940  
; Patent No. 6905686  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/09/724,940  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32

; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: 10-mer peptide  
; OTHER INFORMATION: from A11792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-09-724-940-32

Query Match 68.4%; Score 39; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
DB 1 VGSNKGAI 8

RESULT 20  
US-09-623-548A-958  
; Sequence 958, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjugchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR FILING DATE: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 958  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-623-548A-958

Query Match 68.4%; Score 39; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
DB 3 VGSNKGAI 10

RESULT 21  
US-09-623-548A-964  
; Sequence 964, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjugchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR FILING DATE: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 964  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-964

Query Match 68.4%; Score 39; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
DB 3 VGSNKGAI 10

RESULT 22  
US-09-623-548A-991  
; Sequence 991, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjugchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR FILING DATE: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR FILING DATE: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR FILING DATE: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 991  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-623-548A-991

Query Match 68.4%; Score 39; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
DB 3 VGSNKGAI 10

```
RESULT 23
US-09-657-276-958
; Sequence 958, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 958
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-958
Query Match      68.4%; Score 39; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      3 VGSNKGAI 10

RESULT 24
US-09-657-276-964
; Sequence 964, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 964
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-964
Query Match      68.4%; Score 39; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      3 VGSNKGAI 10

RESULT 25
US-09-657-276-991
; Sequence 991, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 991
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-991
Query Match      68.4%; Score 39; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      3 VGSNKGAI 10

RESULT 26
US-09-623-548A-981
; Sequence 981, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
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; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 981  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-981

Query Match 68.4%; Score 39; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 8 VGSNKGAI 15

RESULT 27  
US-09-623-548A-1008  
; Sequence 1008, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1008  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-1008

Query Match 68.4%; Score 39; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 8 VGSNKGAI 15

RESULT 28  
US-09-657-276-981  
; Sequence 981, Application US/09657276

; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 981  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-981

Query Match 68.4%; Score 39; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
DB 8 VGSNKGAI 15

RESULT 29  
US-09-657-276-1008  
; Sequence 1008, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1008  
; LENGTH: 24  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-1008

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Query Match      68.4%; Score 39; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      8 VGSNKGAI 15

RESULT 30
US-08-304-585-7
; Sequence 7, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Mueiting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueiting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-7

Query Match      68.4%; Score 39; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      15 VGSNKGAI 22

RESULT 31
US-08-609-090-4
; Sequence 4, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-4

Query Match      68.4%; Score 39; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VGSNKGAI 9
      |||||
Db      24 VGSNKGAI 31

RESULT 32
US-08-475-579A-4
; Sequence 4, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggrega
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-475-579A-4

Query Match 68.4%; Score 39; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 18 VGSNKGAI 25

RESULT 33  
US-08-304-585-6  
Sequence 6, Application US/08304585  
Patent No. 5721106  
GENERAL INFORMATION:  
APPLICANT: Maggio, John E.  
APPLICANT: Marfeyh, Patrick W.  
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND  
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.  
STREET: P.O. Box 581415  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55458-1415  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,585  
FILING DATE: 12-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muetting, Ann M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 110.00010120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
US-08-304-585-6

Query Match 68.4%; Score 39; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 24 VGSNKGAI 31

RESULT 34

US-08-612-785B-16  
Sequence 16, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
Aggregation  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Deconci, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-612-785B-16

Query Match 68.4%; Score 39; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 19 VGSNKGAI 26

RESULT 35  
US-08-612-785B-36  
Sequence 36, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
Aggregation  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA

ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-612-785B-36

Query Match 68.4%; Score 39; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 19 VGSNKGAI 26

RESULT 36  
US-08-612-785B-39  
Sequence 39, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-612-785B-39

Query Match 68.4%; Score 39; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 19 VGSNKGAI 26

RESULT 37  
US-08-612-785B-40  
Sequence 40, Application US/08612785B  
Patent No. 5854204  
GENERAL INFORMATION:  
APPLICANT: Findeis, Mark A. et al.  
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,785B  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/404,831  
FILING DATE: 14-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/475,579  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: DeConti, Giulio A.  
REGISTRATION NUMBER: 31,503  
REFERENCE/DOCKET NUMBER: PPI-002CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 35 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-612-785B-40

Query Match 68.4%; Score 39; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 19 VGSNKGAI 26

## RESULT 38

US-08-617-267C-16  
; Sequence 16, Application US/08617267C  
; Patent No. 6319498

; GENERAL INFORMATION:  
; APPLICANT: Findels, Mark A. et al.  
; TITLE OF INVENTION: Modulators of Amyloid Aggregation  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,267C  
; FILING DATE: 14-MAR-1996

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/404,831  
; FILING DATE: 14-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/475,579  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995

; ATTORNEY/AGENT INFORMATION:  
; NAME: DeConti, Giulio A.  
; REGISTRATION NUMBER: 31,503  
; REFERENCE/DOCKET NUMBER: PPI-002CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-617-267C-16

Query Match 68.4%; Score 39; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 19 VGSNKGAI 26

## RESULT 39

US-09-623-548A-979  
; Sequence 979, Application US/09623548A  
; Patent No. 6849714

; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 979  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-623-548A-979

Query Match 68.4%; Score 39; DB 2; Length 35;

Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 19 VGSNKGAI 26

## RESULT 40

US-09-623-548A-1006  
; Sequence 1006, Application US/09623548A  
; Patent No. 6849714

; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; TITLE OF INVENTION: COMPONENTS  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1006  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-1006

Query Match 68.4%; Score 39; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||  
Db 19 VGSNKGAI 26

Search completed: January 28, 2006, 00:59:48  
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 00:58:58 ; Search time 114 Seconds  
(without alignments)  
36.652 Million cell updates/sec

Title: US-09-018-194A-4  
Perfect score: 57  
Sequence: 1 CVGSNKGARC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
\*Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications\_AA\_Main:\*  
1: /cgn2\_6/prodata1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep:\*  
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4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	3	US-09-866-898-4 Sequence 4, Appli
2	57	100.0	10	3	US-09-018-194-4 Sequence 4, Appli
3	57	100.0	10	5	US-10-785-924-4 Sequence 4, Appli
4	43	75.4	123	3	US-09-771-161A-171 Sequence 171, App
5	40	70.2	125	4	US-10-425-115-184821 Sequence 184821
6	39	68.4	8	3	US-09-866-898-1 Sequence 1, Appli
7	39	68.4	8	3	US-09-018-194-1 Sequence 1, Appli
8	39	68.4	8	5	US-10-785-924-1 Sequence 1, Appli
9	39	68.4	9	4	US-10-619-454-12 Sequence 12, Appli
10	39	68.4	9	4	US-10-619-454-131 Sequence 131, App
11	39	68.4	9	4	US-10-619-454-142 Sequence 142, App
12	39	68.4	9	4	US-10-619-454-155 Sequence 155, App
13	39	68.4	10	5	US-10-889-999-30 Sequence 30, Appl
14	39	68.4	10	5	US-10-889-999-31 Sequence 31, Appl
15	39	68.4	10	5	US-10-889-999-32 Sequence 32, Appl
16	39	68.4	10	5	US-10-890-070-30 Sequence 30, Appl
17	39	68.4	10	5	US-10-890-070-31 Sequence 31, Appl
18	39	68.4	10	5	US-10-890-070-32 Sequence 32, Appl
19	39	68.4	10	5	US-10-890-000-30 Sequence 30, Appl
20	39	68.4	10	5	US-10-890-000-31 Sequence 31, Appl
21	39	68.4	10	5	US-10-890-000-32 Sequence 32, Appl
22	39	68.4	10	5	US-10-823-463-30 Sequence 30, Appl
23	39	68.4	10	5	US-10-823-463-31 Sequence 31, Appl
24	39	68.4	10	5	US-10-823-463-32 Sequence 32, Appl
25	39	68.4	10	5	US-10-822-968-30 Sequence 30, Appl
26	39	68.4	10	5	US-10-822-968-31 Sequence 31, Appl
27	39	68.4	10	5	US-10-822-968-32 Sequence 32, Appli

28	39	68.4	10	5	US-10-777-792-30	Sequence 30, Appl
29	39	68.4	10	5	US-10-777-792-31	Sequence 31, Appl
30	39	68.4	10	5	US-10-777-792-32	Sequence 32, Appl
31	39	68.4	10	5	US-10-890-071-30	Sequence 30, Appl
32	39	68.4	10	5	US-10-890-071-31	Sequence 31, Appl
33	39	68.4	10	5	US-10-890-071-32	Sequence 32, Appl
34	39	68.4	10	5	US-10-890-024-30	Sequence 30, Appl
35	39	68.4	10	5	US-10-890-024-31	Sequence 31, Appl
36	39	68.4	10	5	US-10-890-024-32	Sequence 32, Appl
37	39	68.4	10	5	US-10-928-926-30	Sequence 30, Appl
38	39	68.4	10	5	US-10-928-926-31	Sequence 31, Appl
39	39	68.4	10	5	US-10-928-926-32	Sequence 32, Appl
40	39	68.4	10	6	US-11-058-757-30	Sequence 30, Appl
41	39	68.4	10	6	US-11-058-757-31	Sequence 31, Appl
42	39	68.4	10	6	US-11-058-757-32	Sequence 32, Appl
43	39	68.4	11	3	US-09-930-915A-294	Sequence 294, App
44	39	68.4	11	4	US-10-082-014-83	Sequence 83, Appl
45	39	68.4	11	4	US-10-372-076-84	Sequence 84, Appl
46	39	68.4	11	4	US-10-732-862A-97	Sequence 97, Appl
47	39	68.4	11	4	US-10-806-006-294	Sequence 294, App
48	39	68.4	11	4	US-10-677-074-84	Sequence 84, Appl
49	39	68.4	11	4	US-10-805-913-294	Sequence 294, App
50	39	68.4	12	5	US-10-810-881A-118	Sequence 118, App
51	39	68.4	14	5	US-10-997-708-47	Sequence 47, Appl
52	39	68.4	14	5	US-10-997-700-20	Sequence 20, Appl
53	39	68.4	14	6	US-11-066-697-958	Sequence 958, App
54	39	68.4	14	6	US-11-066-697-964	Sequence 964, App
55	39	68.4	14	6	US-11-066-697-991	Sequence 991, App
56	39	68.4	20	3	US-09-792-079-9	Sequence 9, Appli
57	39	68.4	20	4	US-10-159-279-9	Sequence 9, Appli
58	39	68.4	21	3	US-09-792-079-7	Sequence 7, Appli
59	39	68.4	21	4	US-10-159-279-7	Sequence 7, Appli
60	39	68.4	22	3	US-09-792-079-10	Sequence 10, Appl
61	39	68.4	22	4	US-10-159-279-10	Sequence 10, Appl
62	39	68.4	24	5	US-10-728-246-5	Sequence 5, Appli
63	39	68.4	24	5	US-10-728-246-6	Sequence 6, Appli
64	39	68.4	24	6	US-11-066-697-981	Sequence 981, App
65	39	68.4	24	6	US-11-066-697-1008	Sequence 1008, Ap
66	39	68.4	26	3	US-09-792-079-11	Sequence 11, Appl
67	39	68.4	26	4	US-10-159-279-11	Sequence 11, Appl
68	39	68.4	30	5	US-10-625-854-165	Sequence 165, App
69	39	68.4	31	4	US-10-072-602B-567	Sequence 567, App
70	39	68.4	31	5	US-10-625-854-164	Sequence 164, App
71	39	68.4	31	6	US-11-097-315-66	Sequence 66, Appl
72	39	68.4	31	6	US-11-097-315-567	Sequence 567, App
73	39	68.4	32	4	US-10-732-862A-99	Sequence 99, Appl
74	39	68.4	32	5	US-10-625-854-154	Sequence 154, App
75	39	68.4	32	5	US-10-625-854-163	Sequence 163, App
76	39	68.4	33	3	US-09-930-915A-295	Sequence 295, App
77	39	68.4	33	4	US-10-082-014-84	Sequence 84, Appl
78	39	68.4	33	4	US-10-372-076-85	Sequence 85, Appl
79	39	68.4	33	4	US-10-732-862A-98	Sequence 98, Appl
80	39	68.4	33	4	US-10-806-006-295	Sequence 295, App
81	39	68.4	33	4	US-10-677-074-85	Sequence 85, Appl
82	39	68.4	33	4	US-10-805-913-295	Sequence 295, App
83	39	68.4	33	5	US-10-625-854-153	Sequence 153, App
84	39	68.4	33	5	US-10-625-854-162	Sequence 162, App
85	39	68.4	34	5	US-10-625-854-152	Sequence 152, App
86	39	68.4	34	5	US-10-625-854-161	Sequence 161, App
87	39	68.4	35	3	US-09-867-847-3	Sequence 3, Appli
88	39	68.4	35	3	US-09-972-475-16	Sequence 16, Appl
89	39	68.4	35	3	US-10-463-729-16	Sequence 16, Appl
90	39	68.4	35	5	US-10-825-958-3	Sequence 3, Appli
91	39	68.4	35	5	US-10-625-854-151	Sequence 151, App
92	39	68.4	35	5	US-10-625-854-160	Sequence 160, App
93	39	68.4	35	6	US-11-066-697-979	Sequence 979, App
94	39	68.4	35	6	US-11-066-697-1006	Sequence 1006, Ap
95	39	68.4	36	4	US-10-732-862A-436	Sequence 436, App
96	39	68.4	36	5	US-10-625-854-150	Sequence 150, App
97	39	68.4	36	5	US-10-625-854-159	Sequence 159, App
98	39	68.4	37	5	US-10-625-854-149	Sequence 149, App
99	39	68.4	37	5	US-10-625-854-157	Sequence 157, App
100	39	68.4	37	5	US-10-625-854-157	Sequence 157, App

## ALIGNMENTS

RESULT 1  
US-09-866-898-4  
; Sequence 4, Application US/09866898  
; Patent No. US20020051988A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/866,898  
; CURRENT FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: 09/163,095  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic peptide  
US-09-866-898-4  
Query Match 100.0%; Score 57; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CVGSNKGGAIC 10  
DB 1 CVGSNKGGAIC 10  
|||||  
RESULT 2  
US-09-018-194-4  
; Sequence 4, Application US/09018194  
; Publication No. US20030175231A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND  
; TITLE OF INVENTION: COLORATION  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/018,194  
; FILING DATE: 04-FEB-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: US 08/793,683  
; FILING DATE: 30-AUG-1995  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/10971  
; FILING DATE: 30-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/298,941  
; FILING DATE: 31-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hogle, Doreen M.  
; REGISTRATION NUMBER: 36,361  
; REFERENCE/DOCKET NUMBER: BU94-15A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-018-194-4  
Query Match 100.0%; Score 57; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CVGSNKGGAIC 10  
DB 1 CVGSNKGGAIC 10  
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RESULT 3  
US-10-785-924-4  
; Sequence 4, Application US/10785924  
; Publication No. US20040254110A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: 0054.1092-012  
; CURRENT APPLICATION NUMBER: US/10/785,924  
; CURRENT FILING DATE: 2004-02-24  
; PRIOR APPLICATION NUMBER: US 09/866,898  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 09/163,095  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: US 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclic peptide  
US-10-785-924-4  
Query Match 100.0%; Score 57; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CVGSNKGGAIC 10  
DB 1 CVGSNKGGAIC 10  
|||||  
RESULT 4  
US-09-771-161A-171  
; Sequence 171, Application US/09771161A  
; Patent No. US20020110811A1



GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 171  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-171

Query Match 75.4%; Score 43; DB 3; Length 123;  
Best Local Similarity 60.0%; Pred. No. 9;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
DB 100 CKGNRGAVC 109

## RESULT 5

US-10-425-115-184821  
; Sequence 184821, Application US/10425115  
; Publication No. US20040214272A1  
GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cab, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 184821  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_100145C.1.pep  
US-10-425-115-184821

Query Match 70.2%; Score 40; DB 4; Length 125;  
Best Local Similarity 70.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
DB 69 CAGSRYGAI 78

## RESULT 6

US-09-866-898-1  
; Sequence 1, Application US/09866898  
; Patent No. US20020051988A1  
GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: BU96-09A2  
; CURRENT APPLICATION NUMBER: US/09/866,898  
; CURRENT FILING DATE: 2001-05-29

GENERAL INFORMATION:  
; PRIOR APPLICATION NUMBER: 09/163,095  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-898-1

Query Match 68.4%; Score 39; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 1 VGSNKGAI 8

## RESULT 7

US-09-018-194-1  
; Sequence 1, Application US/09018194  
; Publication No. US20030175231A1  
GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaar, Mina  
; APPLICANT: Eller, Mark  
; TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND  
; TITLE OF INVENTION: COLORATION  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/018,194  
; FILING DATE: 04-FEB-1998  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/793,683  
; FILING DATE: 30-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/10971  
; FILING DATE: 30-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/298,941  
; FILING DATE: 31-AUG-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hogle, Doreen M.  
; REGISTRATION NUMBER: 36,361  
; REFERENCE/DOCKET NUMBER: BU94-15A2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 781-861-6240  
; TELEFAX: 781-861-9540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

US-09-018-194-1

Query Match 68.4%; Score 39; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 1 VGSNKGAI 8

RESULT 8

US-10-785-924-1  
; Sequence 1, Application US/10785924  
; Publication No. US2004025410A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrest, Barbara A.  
; APPLICANT: Yaari, Mina  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE  
; FILE REFERENCE: 0054.1092-012  
; CURRENT APPLICATION NUMBER: US/10/785,924  
; CURRENT FILING DATE: 2004-02-24  
; PRIOR APPLICATION NUMBER: US 09/866,898  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 09/163,095  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: PCT/US97/04966  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: US 08/625,765  
; PRIOR FILING DATE: 1996-03-29  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-785-924-1

Query Match 68.4%; Score 39; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 1 VGSNKGAI 8

RESULT 9

US-10-619-454-12  
; Sequence 12, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-12

Query Match 68.4%; Score 39; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 1 VGSNKGAI 8

RESULT 10

US-10-619-454-131  
; Sequence 131, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 131  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-131

Query Match 68.4%; Score 39; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | | | | |  
DB 1 VGSNKGAI 8

RESULT 11

US-10-619-454-142  
; Sequence 142, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Fitzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES  
; TITLE OF INVENTION: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; FILE REFERENCE: P-5202-US  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 142  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-142

Query Match 68.4%; Score 39; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

Db 1 VGSNKGAI 8  
|||||

## RESULT 12

US-10-619-454-155  
; Sequence 155, Application US/10619454  
; Publication No. US20040091945A1  
; GENERAL INFORMATION:  
; APPLICANT: Mindset  
; APPLICANT: Bittzer Attas, Cheryl  
; APPLICANT: Chain, Daniel  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR SCREENING IMMUNOGENIC PEPTIDE VACCINES  
; FILE REFERENCE: AD IN WHICH T-CELL EPITOPES ARE REDUCED  
; CURRENT APPLICATION NUMBER: US/10/619,454  
; CURRENT FILING DATE: 2003-07-16  
; PRIOR APPLICATION NUMBER: US 60/396,245  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 155  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: algorithm generated  
US-10-619-454-155

Query Match 68.4%; Score 39; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||

Db 2 VGSNKGAI 9  
|||||

## RESULT 13

US-10-889-999-30  
; Sequence 30, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||

Db 3 VGSNKGAI 10  
|||||

## RESULT 14

US-10-889-999-31  
; Sequence 31, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||

Db 2 VGSNKGAI 9  
|||||

## RESULT 15

US-10-889-999-32  
; Sequence 32, Application US/10889999  
; Publication No. US20040247590A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/889,999  
; CURRENT FILING DATE: 2004-07-13  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-889-999-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||

Db 1 VGSNKGAI 8

RESULT 16  
US-10-890-070-30  
; Sequence 30, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
Db 3 VGSNKGAI 10

RESULT 17  
US-10-890-070-31  
; Sequence 31, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9

Db 2 VGSNKGAI 9

RESULT 18  
US-10-890-070-32  
; Sequence 32, Application US/108900070  
; Publication No. US20040247591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,070  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-070-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
Db 1 VGSNKGAI 8

RESULT 19  
US-10-890-000-30  
; Sequence 30, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

RESULT 20  
US-10-890-000-31  
; Sequence 31, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 2 VGSNKGAI 9

RESULT 21  
US-10-890-000-32  
; Sequence 32, Application US/10890000  
; Publication No. US20040265301A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,000  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-000-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 1 VGSNKGAI 8

RESULT 22  
US-10-823-463-30  
; Sequence 30, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

RESULT 23  
US-10-823-463-31  
; Sequence 31, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-31

US-10-823-463-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 2 VGSNKGAI 9

RESULT 24  
US-10-823-463-32

; Sequence 32, Application US/10823463  
; Publication No. US20050019328A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nickl  
; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/823,463  
; CURRENT FILING DATE: 2004-04-14  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-823-463-32

US-10-823-463-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 1 VGSNKGAI 8

RESULT 25  
US-10-822-968-30

; Sequence 30, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nickl  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-31

US-10-822-968-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 1 VGSNKGAI 8

RESULT 26  
US-10-822-968-31

; Sequence 31, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nickl  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-30

US-10-822-968-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

RESULT 26

US-10-822-968-31

; Sequence 31, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nickl  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-30

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 2 VGSNKGAI 9

RESULT 27  
US-10-822-968-32  
; Sequence 32, Application US/10822968  
; Publication No. US20050059591A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Vasquez, Nicki  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004750UC  
; CURRENT APPLICATION NUMBER: US/10/822,968  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/580,015  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: US 09/201,430  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
; PRIOR FILING DATE: 1998-11-30  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-822-968-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 1 VGSNKGAI 8

RESULT 28  
US-10-777-792-30  
; Sequence 30, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US

; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 3 VGSNKGAI 10

RESULT 29  
US-10-777-792-31  
; Sequence 31, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 2 VGSNKGAI 9

RESULT 30  
US-10-777-792-32  
; Sequence 32, Application US/10777792  
; Publication No. US20050059802A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US

; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/777,792  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-777-792-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
|||||||  
Db 1 VGSNKGAI 8

RESULT 31  
US-10-890-071-30  
; Sequence 30, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
|||||||  
Db 3 VGSNKGAI 10

RESULT 32  
US-10-890-071-31  
; Sequence 31, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
|||||||  
Db 2 VGSNKGAI 9

RESULT 33  
US-10-890-071-32  
; Sequence 32, Application US/108900071  
; Publication No. US20050123544A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004760US  
; CURRENT APPLICATION NUMBER: US/10/890,071  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: US/09/580,018  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
; OTHER INFORMATION: peptide)  
US-10-890-071-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
|||||||  
Db 1 VGSNKGAI 8

RESULT 34  
US-10-890-024-30  
; Sequence 30, Application US/108900024  
; Publication No. US20050158304A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Bard, Frederique



APPLICANT: Yednock, Ted  
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
FILE REFERENCE: 15270J-004760US  
CURRENT APPLICATION NUMBER: US/10/890,024  
CURRENT FILING DATE: 2004-07-12  
PRIOR APPLICATION NUMBER: US/09/580,018  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
OTHER INFORMATION: peptide)  
US-10-890-024-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
DB 3 VGSNKGAI 10

RESULT 35  
US-10-890-024-31  
Sequence 31, Application US/10890024  
Publication No. US20050158304A1  
GENERAL INFORMATION:  
APPLICANT: Schenk, Dale B.  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
FILE REFERENCE: 15270J-004760US  
CURRENT APPLICATION NUMBER: US/10/890,024  
CURRENT FILING DATE: 2004-07-12  
PRIOR APPLICATION NUMBER: US/09/580,018  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
OTHER INFORMATION: peptide)  
US-10-890-024-31

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
DB 2 VGSNKGAI 9

RESULT 36  
US-10-890-024-32  
Sequence 32, Application US/10890024  
Publication No. US20050158304A1  
GENERAL INFORMATION:  
APPLICANT: Schenk, Dale B.

APPLICANT: Bard, Frederique  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
FILE REFERENCE: 15270J-004760US  
CURRENT APPLICATION NUMBER: US/10/890,024  
CURRENT FILING DATE: 2004-07-12  
PRIOR APPLICATION NUMBER: US/09/580,018  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 32  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
OTHER INFORMATION: peptide)  
US-10-890-024-32

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
DB 1 VGSNKGAI 8

RESULT 37  
US-10-928-926-30  
Sequence 30, Application US/10928926  
Publication No. US20050196399A1  
GENERAL INFORMATION:  
APPLICANT: Schenk, Dale B.  
APPLICANT: Bard, Frederique  
APPLICANT: Vasquez, Nicki  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
FILE REFERENCE: 15270J-004750UC  
CURRENT APPLICATION NUMBER: US/10/928,926  
CURRENT FILING DATE: 2004-08-27  
PRIOR APPLICATION NUMBER: US/09/724,961  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 09/580,015  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: US 09/201,430  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: WO PCT/US00/14810  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: US 60/080,970  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: US 60/067,740  
PRIOR FILING DATE: 1997-12-02  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide  
OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid  
OTHER INFORMATION: peptide)  
US-10-928-926-30

Query Match 68.4%; Score 39; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 VGSNKGAI 9
      |||||
Db      3 VGSNKGAI 10

RESULT 38
US-10-928-926-31
; Sequence 31, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-928-926-31

Query Match      68.4%; Score 39; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
      |||||
Db      2 VGSNKGAI 9

RESULT 39
US-10-928-926-32
; Sequence 32, Application US/10928926
; Publication No. US20050196399A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/10/928,926
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/09/724,961
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
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; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-10-928-926-32

Query Match      68.4%; Score 39; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
      |||||
Db      1 VGSNKGAI 8

RESULT 40
US-11-058-757-30
; Sequence 30, Application US/11058757
; Publication No. US20050142132A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/11/058,757
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
; US-11-058-757-30

Query Match      68.4%; Score 39; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
      |||||
Db      3 VGSNKGAI 10
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Search completed: January 28, 2006, 01:09:46  
Job time : 118 secs

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OM protein - protein search, using sw model

Run on: January 28, 2006, 00:59:24 ; Search time 32 Seconds  
(without alignments)  
3.384 Million cell updates/sec

Title: US-09-018-194A-4  
Perfect score: 57  
Sequence: 1 CVGSNKGARC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 75621

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:  
2: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:  
3: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:  
4: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:  
5: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep:  
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7: /cgn2\_6/prodata/2/pubpaa/US11\_NEW\_PUB.pep:  
8: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	68.4	40	6	US-10-250-581-3
2	39	68.4	40	6	US-10-250-581-6
3	39	68.4	40	6	US-10-250-581-9
4	39	68.4	40	6	US-10-250-581-12
5	39	68.4	40	6	US-10-250-581-15
6	39	68.4	40	6	US-10-250-581-18
7	39	68.4	40	6	US-10-250-581-3
8	39	68.4	40	6	US-10-250-581-6
9	39	68.4	40	6	US-10-250-581-9
10	39	68.4	40	6	US-10-250-581-12
11	39	68.4	40	6	US-10-250-581-15
12	39	68.4	40	6	US-10-250-581-18
13	39	68.4	40	7	US-11-016-706-36
14	39	68.4	42	6	US-10-923-605-1
15	39	68.4	42	6	US-10-934-818-1
16	39	68.4	42	6	US-10-250-581-4
17	39	68.4	42	6	US-10-250-581-7
18	39	68.4	42	6	US-10-250-581-10
19	39	68.4	42	6	US-10-250-581-13
20	39	68.4	42	6	US-10-250-581-16
21	39	68.4	42	6	US-10-250-581-19
22	39	68.4	42	6	US-10-250-581-4
23	39	68.4	42	6	US-10-250-581-7
24	39	68.4	42	6	US-10-250-581-10
25	39	68.4	42	6	US-10-250-581-13
26	39	68.4	42	6	US-10-250-581-16
27	39	68.4	42	6	US-11-016-706-37
28	39	68.4	42	7	US-11-031-538-1
29	39	68.4	42	6	US-10-934-818-6
30	39	68.4	43	6	US-10-250-581-1
31	39	68.4	43	6	US-10-250-581-1
32	39	68.4	43	6	US-10-250-581-1
33	39	68.4	43	6	US-10-677-076-2
34	39	68.4	103	6	US-10-677-076-2
35	39	68.4	770	6	US-10-982-545-15
36	39	68.4	770	6	US-10-789-273-38
37	35	61.4	30	7	US-11-174-996A-7
38	35	61.4	30	7	US-11-174-996A-22
39	35	61.4	260	6	US-10-131-826A-396
40	35	61.4	260	6	US-10-510-321-2
41	35	61.4	260	7	US-11-183-914-7
42	35	61.4	545	6	US-10-063-703-110
43	35	61.4	545	7	US-11-102-240-110
44	33	57.9	63	7	US-11-174-996A-51
45	33	57.9	223	6	US-10-878-556A-167
46	33	57.9	1076	6	US-10-131-826A-219
47	33	57.9	3500	7	US-11-085-775-2
48	32	56.1	116	6	US-10-689-742-222
49	32	56.1	503	6	US-10-453-372-1038
50	32	56.1	760	7	US-11-052-554A-68
51	32	56.1	794	7	US-11-024-959-478
52	32	56.1	2725	7	US-11-113-424-52
53	31	54.4	19	6	US-10-923-605-5
54	31	54.4	19	6	US-10-934-818-5
55	31	54.4	30	7	US-11-174-996A-16
56	31	54.4	1068	6	US-10-467-657-2904
57	31	54.4	1268	6	US-10-453-372-1144
58	31	54.4	1268	6	US-10-453-372-1154
59	31	54.4	1288	6	US-10-453-372-1146
60	31	54.4	1288	6	US-10-453-372-1152
61	31	54.4	1368	6	US-10-770-303-2
62	31	54.4	1368	7	US-11-185-372-2
63	31	54.4	30	7	US-11-174-996A-13
64	30	52.6	30	7	US-11-174-996A-14
65	30	52.6	30	7	US-11-174-996A-15
66	30	52.6	30	7	US-11-174-996A-17
67	30	52.6	30	7	US-11-174-996A-18
68	30	52.6	30	7	US-11-174-996A-19
69	30	52.6	30	7	US-11-174-996A-21
70	30	52.6	30	7	US-11-174-996A-23
71	30	52.6	76	7	US-11-174-996A-63
72	30	52.6	259	6	US-10-631-558-4
73	30	52.6	300	7	US-11-006-119-31
74	30	52.6	308	6	US-10-821-234-1001
75	30	52.6	447	6	US-10-967-527A-14
76	30	52.6	604	6	US-10-453-372-1160
77	30	52.6	622	6	US-10-453-372-1184
78	30	52.6	642	6	US-10-995-561-631
79	30	52.6	657	6	US-10-995-561-632
80	30	52.6	685	6	US-10-467-657-2302
81	30	52.6	885	6	US-10-995-561-629
82	30	52.6	984	6	US-10-467-657-1820
83	30	52.6	1144	6	US-10-453-372-1188
84	30	52.6	1544	6	US-10-453-372-1186
85	30	52.6	1565	6	US-10-453-372-1180
86	30	52.6	1566	6	US-10-453-372-1190
87	30	52.6	2053	6	US-10-453-372-1174
88	30	52.6	2143	6	US-10-453-372-1188
89	30	52.6	2296	6	US-10-995-561-633
90	30	52.6	2355	6	US-10-995-561-627
91	30	52.6	2355	6	US-10-821-234-1545
92	30	52.6	2384	6	US-10-821-234-1545
93	30	52.6	2386	6	US-10-995-561-626
94	29	50.9	30	7	US-11-174-996A-3
95	29	50.9	30	7	US-11-174-996A-8
96	29	50.9	30	7	US-11-174-996A-10
97	29	50.9	49	6	US-10-467-657-4058
98	29	50.9	67	6	US-10-467-657-1834

99 29 50.9 75 6 US-10-478-345-12 Sequence 12, Appl  
100 29 50.9 75 7 US-11-174-996A-87 Sequence 87, Appl

## ALIGNMENTS

## RESULT 1

US-10-250-581-3

; Sequence 3, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 3

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-3

Query Match

Best Local Similarity 68.4%; Score 39; DB 6; Length 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

## RESULT 2

US-10-250-581-6

; Sequence 6, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 6

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-6

Query Match

Best Local Similarity 68.4%; Score 39; DB 6; Length 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

## RESULT 3

US-10-250-581-9

; Sequence 15, Application US/10250581

; Sequence 9, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 9

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (21)

; OTHER INFORMATION: Xaa=Orn

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-9

Query Match

Best Local Similarity 68.4%; Score 39; DB 6; Length 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

## RESULT 4

US-10-250-581-12

; Sequence 12, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 12

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (21)

; OTHER INFORMATION: Xaa=Dab

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-12

Query Match

Best Local Similarity 68.4%; Score 39; DB 6; Length 40;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

## RESULT 5

US-10-250-581-15

; Sequence 15, Application US/10250581

```
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ....
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match      68.4%; Score 39; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
Db      24 VGSNKGAI 31

RESULT 6
US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ....
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa-Dab
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match      68.4%; Score 39; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
Db      24 VGSNKGAI 31

RESULT 7
US-10-250-581-3
; Sequence 3, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ....
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-3

Query Match      68.4%; Score 39; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
Db      24 VGSNKGAI 31

RESULT 8
US-10-250-581-6
; Sequence 6, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ....
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 6
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-6

Query Match      68.4%; Score 39; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
Db      24 VGSNKGAI 31

RESULT 9
US-10-250-581-9
; Sequence 9, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ....
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-9

Query Match      68.4%; Score 39; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      2 VGSNKGAI 9
Db      24 VGSNKGAI 31
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; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-9

Query Match 68.4%; Score 39; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 24 VGSNKGAI 31

RESULT 10  
US-10-250-581-12  
; Sequence 12, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 12  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-12

Query Match 68.4%; Score 39; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 24 VGSNKGAI 31

RESULT 11  
US-10-250-581-15  
; Sequence 15, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 15  
; LENGTH: 40

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-15

Query Match 68.4%; Score 39; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 24 VGSNKGAI 31

RESULT 12  
US-10-250-581-18  
; Sequence 18, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 18  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-18

Query Match 68.4%; Score 39; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||  
Db 24 VGSNKGAI 31

RESULT 13  
US-11-016-706-36  
; Sequence 36, Application US/11016706  
; Publication No. US20050244334A1  
; GENERAL INFORMATION:  
; APPLICANT: CASTILLO, GERARDO  
; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-016-706-36

Query Match 68.4%; Score 39; DB 7; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 14  
US-10-923-605-1  
; Sequence 1, Application US/10923605  
; Publication No. US20050249727A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-004740US  
; CURRENT APPLICATION NUMBER: US/10/923,605  
; CURRENT FILING DATE: 2004-08-20  
; PRIOR APPLICATION NUMBER: US/09/322,289  
; PRIOR FILING DATE: 1999-05-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-923-605-1

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 15  
US-10-934-818-1  
; Sequence 1, Application US/10934818  
; Publication No. US20050255122A1  
; GENERAL INFORMATION:  
; APPLICANT: Schenk, Dale B.  
; APPLICANT: Neuralab Limited  
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease  
; FILE REFERENCE: 15270J-472000US  
; CURRENT APPLICATION NUMBER: US/10/934,818  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 60/067,740  
; PRIOR FILING DATE: 1997-12-02  
; PRIOR APPLICATION NUMBER: US 60/080,970  
; PRIOR FILING DATE: 1998-04-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1

; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide  
US-10-934-818-1

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 16  
US-10-250-581-4  
; Sequence 4, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 4  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-4

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 17  
US-10-250-581-7  
; Sequence 7, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 7  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-7

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 24 VGSNKGAI 31

RESULT 18  
US-10-250-581-10  
; Sequence 10, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 10  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-10

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 24 VGSNKGAI 31

RESULT 19  
US-10-250-581-13  
; Sequence 13, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 13  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-13

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 24 VGSNKGAI 31

RESULT 20  
US-10-250-581-16  
; Sequence 16, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 16  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-16

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 24 VGSNKGAI 31

RESULT 21  
US-10-250-581-19  
; Sequence 19, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 19  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-19

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 22  
US-10-250-581-4  
; Sequence 4, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 4  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-4

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 23  
US-10-250-581-7  
; Sequence 7, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 7  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-7

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 24  
US-10-250-581-10  
; Sequence 10, Application US/10250581  
; Publication No. US20040116337A1

; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 10  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Orn  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-10

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 25  
US-10-250-581-13  
; Sequence 13, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs....  
; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581  
; CURRENT FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Version 2.1  
; SEQ ID NO 13  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (21)  
; OTHER INFORMATION: Xaa=Dab  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (17)..(21)  
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are  
; OTHER INFORMATION: linked together through an intramolecular bridge.  
US-10-250-581-13

Query Match 68.4%; Score 39; DB 6; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.38;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 24 VGSNKGAI 31

RESULT 26  
US-10-250-581-16  
; Sequence 16, Application US/10250581  
; Publication No. US20040116337A1  
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...  
; TITLE OF INVENTION: Soluble cyclic analogs...

; FILE REFERENCE: 16069  
; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 16

; LENGTH: 42

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: PEPTIDE

; LOCATION: (17)

; OTHER INFORMATION: Xaa=Orn

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-16

Query Match 68.4%; Score 39; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

RESULT 27

US-10-250-581-19

; Sequence 19, Application US/10250581

; Publication No. US20040116337A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...

; TITLE OF INVENTION: Soluble cyclic analogs...

; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1

; SEQ ID NO 19

; LENGTH: 42

; TYPE: PRT

; ORGANISM: Homo sapiens

; NAME/KEY: PEPTIDE

; LOCATION: (17)

; OTHER INFORMATION: Xaa=Dab

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (17)..(21)

; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are

; OTHER INFORMATION: linked together through an intramolecular bridge.

US-10-250-581-19

Query Match 68.4%; Score 39; DB 6; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

RESULT 28

US-11-016-706-37

; Sequence 37, Application US/11016706

; Publication No. US20050244334A1

; GENERAL INFORMATION:

; APPLICANT: CASTILLO, GERARDO

; APPLICANT: LAKE, THOMAS P.  
; APPLICANT: NGUYEN, BETH P.  
; APPLICANT: SANDERS, VIRGINIA J.  
; APPLICANT: SNOW, ALAN D.  
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND  
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS  
; FILE REFERENCE: PROTEO.P03C13  
; CURRENT APPLICATION NUMBER: US/11/016,706  
; CURRENT FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 09/962,955  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/938,275  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 08/947,057  
; PRIOR FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: Patent In Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; US-11-016-706-37

Query Match 68.4%; Score 39; DB 7; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

RESULT 29

US-11-031-538-1

; Sequence 1, Application US/11031538

; Publication No. US20060009433A1

; GENERAL INFORMATION:

; APPLICANT: Yao, Zhi-Xing

; APPLICANT: Lecanu, Laurent

; APPLICANT: Teper, Gary L.

; APPLICANT: Greeson, Janet

; APPLICANT: Papadopoulos, Vassilios

; APPLICANT: Samaritan Pharmaceuticals, Inc.

; TITLE OF INVENTION: Neuroprotective Spirostenol Pharmaceutical Compositions

; FILE REFERENCE: 1941.023WO1

; CURRENT APPLICATION NUMBER: US/11/031,538

; CURRENT FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: US 10/389,189

; PRIOR FILING DATE: 2003-03-14

; PRIOR APPLICATION NUMBER: US 10/663,619

; PRIOR FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US 60/364,140

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: US 60/319,846

; PRIOR FILING DATE: 2003-01-09

; PRIOR APPLICATION NUMBER: US 60/618,696

; PRIOR FILING DATE: 2004-10-14

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 42

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-031-538-1

Query Match 68.4%; Score 39; DB 7; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

|||||

Db 24 VGSNKGAI 31

```

; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 33
US-10-677-076-1
; Sequence 1, Application US/10677076
; Publication No. US20060014696A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid
; Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/677,076
; FILING DATE: 30-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162
; FILING DATE: 27-AUG-1997
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-677-076-1

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 32
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 31
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 30
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 31
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      68.4%; Score 39; DB 6; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGAI 9
DB      24 VGSNKGAI 31

RESULT 32
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs...
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
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QY      2 VGSNKGA1 9
Db      24 VGSNKGA1 31

RESULT 34
US-10-677-076-2
; Sequence 2, Application US/10677076
; Publication No. US20060014696A1
; GENERAL INFORMATION:
; APPLICANT: Findels, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid
; Peptide
; Aggregation Comprising D-Amino Acids
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/677,076
; FILING DATE: 30-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162
; FILING DATE: 27-AUG-1997
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-677-076-2
Query Match      68.4%; Score 39; DB 6; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VGSNKGA1 9
Db      28 VGSNKGA1 35

RESULT 35
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PPT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; FEATURE:
; OTHER INFORMATION: signal peptide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-N1), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
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OTHER INFORMATION: P3(42)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(711)  
OTHER INFORMATION: P3(40)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (712)..(770)  
OTHER INFORMATION: gamma-CTF(59)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (714)..(770)  
OTHER INFORMATION: gamma-CTF(57)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (721)..(770)  
OTHER INFORMATION: gamma-CTF(50)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (740)..(770)  
OTHER INFORMATION: C31  
US-10-982-545-15

Query Match 68.4%; Score 39; DB 6; Length 770;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 695 VGSNKGAI 702  
|||||||

RESULT 36  
US-10-789-273-38  
Sequence 38, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Basi, Gurik  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
CURRENT FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-789-273-38

Query Match 68.4%; Score 39; DB 6; Length 770;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 695 VGSNKGAI 702  
|||||||

RESULT 37  
US-11-174-996A-7  
Sequence 7, Application US/11174996A  
Publication No. US20060014673A1  
GENERAL INFORMATION:

APPLICANT: Layer, Richard T.  
APPLICANT: Pemberton, Karen E.  
APPLICANT: Jones, Robert M.  
APPLICANT: Garrett, James L.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Hilliard, David R.  
APPLICANT: Grilley, Michelle  
APPLICANT: Watkins, Maren  
APPLICANT: Santos, Ameurfina D.  
APPLICANT: Zafaralla, Glenn  
APPLICANT: Craig, A. Grey  
APPLICANT: Cognetix, Inc.  
APPLICANT: University of Utah Research Foundation  
APPLICANT: The Salk Institute for Biological Studies  
TITLE OF INVENTION: Kappa-A Conopeptides and Uses Therefor  
FILE REFERENCE: 2314-294  
CURRENT APPLICATION NUMBER: US/11/174,996A  
CURRENT FILING DATE: 2005-07-06  
PRIOR APPLICATION NUMBER: US 10/139,272  
PRIOR FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: US 09/413,354  
PRIOR FILING DATE: 1999-10-06  
PRIOR APPLICATION NUMBER: US 60/103,247  
PRIOR FILING DATE: 1998-10-06  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 30  
TYPE: PRT  
ORGANISM: Conus consors  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (2)..(22)  
OTHER INFORMATION: Xaa at residues 2, 6, 17 and 22 is Pro or hydroxy-Pro;  
OTHER INFORMATION: Xaa at residue 3 is Trp, D-Trp or breomo-Trp; Xaa at  
OTHER INFORMATION: residue 15 is Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
OTHER INFORMATION: O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.  
US-11-174-996A-7

Query Match 61.4%; Score 35; DB 7; Length 30;  
Best Local Similarity 50.0%; Pred. No. 1.5;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
Db 12 CCGXNKGIMC 21  
|||||||

RESULT 38  
US-11-174-996A-22  
Sequence 22, Application US/11174996A  
Publication No. US20060014673A1  
GENERAL INFORMATION:  
APPLICANT: Layer, Richard T.  
APPLICANT: Pemberton, Karen E.  
APPLICANT: Jones, Robert M.  
APPLICANT: Garrett, James L.  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: McIntosh, J. Michael  
APPLICANT: Hilliard, David R.  
APPLICANT: Grilley, Michelle  
APPLICANT: Watkins, Maren  
APPLICANT: Santos, Ameurfina D.  
APPLICANT: Zafaralla, Glenn  
APPLICANT: Craig, A. Grey  
APPLICANT: Cognetix, Inc.  
APPLICANT: University of Utah Research Foundation  
APPLICANT: The Salk Institute for Biological Studies  
TITLE OF INVENTION: Kappa-A Conopeptides and Uses Therefor  
FILE REFERENCE: 2314-294  
CURRENT APPLICATION NUMBER: US/11/174,996A  
CURRENT FILING DATE: 2005-07-06

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; PRIOR APPLICATION NUMBER: US 10/139,272
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/413,354
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: US 60/103,247
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus aurisiacus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (2)..(23)
; OTHER INFORMATION: Xaa at residues 2, 6, 17, 22 and 23 is Pro or hydroxy-
; OTHER INFORMATION: Pro; Xaa at residue 3 is Trp, D-Trp or bromo-Trp;
; OTHER INFORMATION: Xaa at residue 15 is Trp, mono-iodo-Trp, di-iodo-Trp,
; OTHER INFORMATION: O-sulpho-Trp, O-phospho-Trp or nitro-Trp.
US-11-174-996A-22

Query Match          61.4%; Score 35; DB 7; Length 30;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CVGSKNGAIC 10
Db      12 CCGXKXGTC 21

RESULT 39
US-10-131-826A-396
; Sequence 396, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 396
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-826A-396

Query Match          61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CVGSKNGKA 8
Db      198 CAGSSKGA 205

RESULT 40
US-10-510-321-2
; Sequence 2, Application US/10510321
; Publication No. US20050287528A1
; GENERAL INFORMATION:
; APPLICANT: Kishi, Tadaaki
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: Methods for Detecting Ovarian Cancer
; FILE REFERENCE: 11757.104USWO
; CURRENT APPLICATION NUMBER: US/10/510,321
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/CA03/00495
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,559
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-321-2

Query Match          61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CVGSKNGKA 8
Db      198 CAGSSKGA 205

Search completed: January 28, 2006, 01:10:28
Job time : 33 secs
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 28, 2006, 00:54:21 ; Search time 16 Seconds  
(without alignments)  
60.135 Million cell updates/sec

Title: US-09-018-194A-4  
Perfect score: 57  
Sequence: 1 CVGSNKGARIC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 80:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	70.2	284	2 F82666	phage-related prot
2	39	68.4	42	2 PNO512	beta-amyloid prote
3	39	68.4	57	2 A60045	Alzheimer's diseas
4	39	68.4	57	2 F60045	Alzheimer's diseas
5	39	68.4	57	2 D60045	Alzheimer's diseas
6	39	68.4	57	2 E60045	Alzheimer's diseas
7	39	68.4	57	2 G60045	Alzheimer's diseas
8	39	68.4	57	2 B60045	Alzheimer's diseas
9	39	68.4	82	2 PQ0438	Alzheimer's diseas
10	39	68.4	695	1 A49795	Alzheimer's diseas
11	39	68.4	695	2 A27485	Alzheimer's diseas
12	39	68.4	695	2 S00550	Alzheimer's diseas
13	39	68.4	747	2 JH0773	Alzheimer's diseas
14	39	68.4	770	1 QRH044	Alzheimer's diseas
15	38	66.7	372	2 T29359	hypothetical prote
16	37	64.9	89	2 T26222	hypothetical prote
17	37	64.9	556	2 H69279	adenine deaminase
18	36	63.2	474	2 H69185	amidophosphoribos
19	36	63.2	1088	2 A63493	cysteine proteinase
20	36	63.2	1555	2 T18688	hypothetical prote
21	36	63.2	1973	2 G89608	protein B0272.5 [i
22	36	63.2	1973	2 T18686	hypothetical prote
23	35	61.4	299	2 F95294	probable Lysr-type
24	35	61.4	473	2 A56175	adhesive plaque pr
25	35	61.4	786	2 H69980	single-strand DNA-
26	34	59.6	87	2 A38725	transferrin - shee
27	34	59.6	191	2 T19573	hypothetical prote
28	34	59.6	191	2 T22036	hypothetical prote
29	34	59.6	316	2 E71812	transaldolase - He

30	59.6	316	2	G64706	transaldolase - He
31	59.6	356	2	T22998	hypothetical prote
32	59.6	426	2	T51506	hypothetical prote
33	59.6	457	1	G70116	histidine-tRNA lig
34	59.6	470	2	T45816	hypothetical prote
35	59.6	611	2	S76211	hypothetical prote
36	59.6	615	2	T20839	hypothetical prote
37	59.6	640	2	T19346	hypothetical prote
38	59.6	644	2	B71409	hypothetical prote
39	59.6	661	1	A42287	phosphoprotein pho
40	59.6	661	2	T42754	hypothetical prote
41	59.6	752	2	AD2076	methyl-accepting c
42	59.6	795	2	T52516	hypothetical prote
43	59.6	797	2	S28103	probable DNA-direc
44	59.6	1391	2	T20406	hypothetical prote
45	59.6	1628	2	T43682	nucleoporin - fiss
46	58.8	1106	1	A39299	DNA-directed DNA p
47	58.8	1107	1	A41618	DNA-directed DNA p
48	57.9	69	2	A83044	histone-like DNA-b
49	57.9	170	2	S43476	hypothetical 19.4K
50	57.9	173	2	S20689	hypothetical prote
51	57.9	186	2	B90116	hemiferrin - bovin
52	57.9	215	2	A60166	hemiferrin - rat
53	57.9	216	1	A39684	nucleoside-triphos
54	57.9	223	1	KIHUA3	hypothetical prote
55	57.9	303	2	S45461	aryl hydrocarbon r
56	57.9	358	2	S58376	aryl hydrocarbon n
57	57.9	392	2	JC7633	probable ATP-bindi
58	57.9	392	2	A82974	ATP-dependent 26S
59	57.9	430	2	G64446	hypothetical prote
60	57.9	442	2	T06640	hypothetical prote
61	57.9	487	2	T27069	hypothetical prote
62	57.9	497	2	I70147	gene P2A B protei
63	57.9	776	2	A55448	An receptor nuclea
64	57.9	789	2	I59550	aryl hydrocarbon r
65	57.9	791	2	A56241	aryl hydrocarbon r
66	57.9	805	2	JC7635	aryl hydrocarbon r
67	57.9	963	2	B83502	ribonucleoside red
68	57.9	1047	2	F81728	ribonucleoside-dip
69	57.9	1053	2	D71466	probable ribonucle
70	57.9	1110	1	B42544	G2-G1 polypeptid
71	57.9	1616	2	S62504	conserved hypothet
72	57.9	1869	2	A59290	class V chitin syn
73	57.9	7962	2	I38346	elastic chitin - hu
74	56.1	106	2	C86086	hypothetical prote
75	56.1	138	2	B93365	hypothetical prote
76	56.1	161	2	H71677	invasion protein A
77	56.1	192	2	T22142	hypothetical prote
78	56.1	210	2	G95858	probable 3-octapre
79	56.1	219	2	I52644	neuronal protein -
80	56.1	264	2	S10318	proteasome endopep
81	56.1	264	2	D85097	hypothetical prote
82	56.1	292	1	A39871	calponin alpha, sm
83	56.1	295	2	E97329	sugar kinase, ribo
84	56.1	297	1	JN0773	calponin H1 - rat
85	56.1	297	1	S31484	calponin H1 - pig
86	56.1	297	1	S31486	calponin H1 - mous
87	56.1	297	2	JC4500	basic calponin - h
88	56.1	297	2	G02142	smooth muscle cell
89	56.1	325	2	AD1871	fructokinase (limp
90	56.1	349	2	A75169	probable iron (III
91	56.1	359	2	H65201	pts system, fructo
92	56.1	361	2	AC0050	protein-Npi-phosph
93	56.1	375	2	A71625	rikin PFB0035C - m
94	56.1	377	2	G69937	lipopolysaccharide
95	56.1	404	2	G97888	hypothetical prote
96	56.1	442	1	S36204	probable beta-keto
97	56.1	454	2	T48005	hypothetical prote
98	56.1	475	2	JQ2214	1-aminocyclopropan
99	56.1	483	2	C64231	proline-tRNA ligas
100	56.1	490	2	S31450	1-aminocyclopropan

ALIGNMENTS

RESULT 1  
F82666  
phage-related protein XF1555 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82666  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: F82666  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-284 <SIM>  
A:Cross-references: UNIPROT:Q9PD24; UNIPARC:UPI00000C277B; GB:AE003985; GB:AE003849; NID  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigh  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1555

Query Match 70.2%; Score 40; DB 2; Length 284;  
Best Local Similarity 60.0%; Pred. No. 7.4;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CVGSNKGAI 10  
||| : |||  
Db 248 CVGDDGALC 257

RESULT 2  
PN0512  
beta-amyloid protein - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: PN0512  
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M  
Biochem. Biophys. Res. Commun. 193, 624-630, 1993  
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragme  
A:Reference number: PN0512; MUID:93290853; PMID:768598  
A:Accession: PN0512  
A:Molecule type: protein  
A:Residues: 1-42 <SHI>  
A:Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; amyloid

Query Match 68.4%; Score 39; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 VGSNKGAI 9  
|||||||  
Db 24 VGSNKGAI 31

RESULT 3

A60045  
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: A60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: A60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI00000125049; EMBL:X56125  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain  
Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 VGSNKGAI 9  
|||||||  
Db 29 VGSNKGAI 36  
RESULT 4  
F60045  
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 13-Aug-1999  
C:Accession: F60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: F60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI00000125049; EMBL:X56127; NID:gl1895; PIDN:CAA39592.1; PID:  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain  
Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 VGSNKGAI 9  
|||||||  
Db 29 VGSNKGAI 36  
RESULT 5  
D60045  
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: D60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: D60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI00000125049; EMBL:X56124  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain  
Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 VGSNKGAI 9



Db 29 VGSNKGAI 36  
|||||

## RESULT 6

E60045  
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)  
C:Species: Ovis sp. (sheep)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: E60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: E60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56130  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9  
|||||

Db 29 VGSNKGAI 36

## RESULT 7

G60045  
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 28-Jul-1995  
C:Accession: G60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: G60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56126  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9  
|||||

Db 29 VGSNKGAI 36

## RESULT 8

B60045  
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)  
C:Species: Ursus maritimus (polar bear)  
C:Date: 01-Dec-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: B60045  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: B60045  
A:Molecule type: mRNA  
A:Residues: 1-57 <JOH>  
A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:g2165; PIDN:  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;  
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9  
|||||

Db 29 VGSNKGAI 36

## RESULT 9

PQ0438  
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Sep-1993 #sequence\_revision 19-Oct-1995 #text\_change 19-Oct-1995  
C:Accession: PQ0438; C60045  
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.  
Biochem. Biophys. Res. Commun. 188, 905-911, 1992  
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor  
A:Reference number: PQ0438; MUID:93075180; PMID:1445331  
A:Accession: PQ0438  
A:Molecule type: DNA  
A:Residues: 1-82 <DAV>  
A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657  
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.  
Brain Res. Mol. Brain Res. 10, 299-305, 1991  
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,  
A:Reference number: A60045; MUID:92017079; PMID:1656157  
A:Accession: C60045  
A:Molecule type: mRNA  
A:Residues: 12-68 <JOH>  
A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 68.4%; Score 39; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9  
|||||

Db 40 VGSNKGAI 47

## RESULT 10

A49795  
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A49795  
R:Podlasky, M.B.; Tolan, D.R.; Selkoe, D.J.  
Am. J. Pathol. 138, 1423-1435, 1991  
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a  
A:Reference number: A49795; MUID:91273117; PMID:1905108  
A:Accession: A49795  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-695 <POD>  
A:Cross-references: UNIPARC:UPI000002A3F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:  
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C:Keywords: alternative splicing

Query Match 68.4%; Score 39; DB 1; Length 695;  
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9  
|||||

Db 620 VGSNKGAI 627

## RESULT 11

A27485  
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse

N;/Alternate names: proteinase nexin II  
C;/Species: Mus musculus (house mouse)  
C;/Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004  
C;/Accession: A27485; S19727; I49485  
R;/Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.  
Biochem. Biophys. Res. Commun. 149, 665-671, 1987  
A;/Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor  
A;/Reference number: A27485; MUID:88106489; PMID:3322280  
A;/Accession: A27485  
A;/Molecule type: mRNA  
A;/Residues: 1-695 <YAM>  
A;/Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:  
A;/Experimental source: brain  
R;/de Strooper, B.; van Leuven, F.; van den Berghe, H.  
Biochim. Biophys. Acta 1129, 141-143, 1991  
A;/Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer  
A;/Reference number: S19727; MUID:92096458; PMID:1756177  
A;/Accession: S19727  
A;/Molecule type: mRNA  
A;/Residues: 1-210,'G',212-220,'S',222-396,'A',398-402,'T',404-448,'A',450-695 <STR>  
A;/Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379  
R;/Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.  
Gene 112, 189-195, 1992  
A;/Title: Positive and negative regulatory elements for the expression of the Alzheimer's  
A;/Reference number: I49485; MUID:92209998; PMID:1555768  
A;/Accession: I49485  
A;/Status: translated from GB/EMBL/DBJ  
A;/Molecule type: DNA  
A;/Residues: 1-19 <RES>  
A;/Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:  
C;/Genetics:  
A;/Map position: 16C3  
C;/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;/Keywords: alternative splicing; amyloid; transmembrane protein  
Query Match 68.4%; Score 39; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 620 VGSNKGAI 627  
|||||  
RESULT 12  
S00550  
Alzheimer's disease amyloid beta protein precursor - rat  
N;/Alternate names: beta-A4 amyloid protein  
C;/Species: Rattus norvegicus (Norway rat)  
C;/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C;/Accession: S00550; A41245; A39820; S46251  
R;/Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.  
EMBO J. 7, 1365-1370, 1988  
A;/Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain  
A;/Reference number: S00550; MUID:88312583; PMID:2900758  
A;/Accession: S00550  
A;/Molecule type: mRNA  
A;/Residues: 1-695 <SHI>  
A;/Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648; NID:g55616; PIDN:  
R;/Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.  
Science 241, 223-226, 1988  
A;/Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core  
A;/Reference number: A41245; MUID:88264430; PMID:2968652  
A;/Accession: A41245  
A;/Molecule type: protein  
A;/Residues: 18-37,'X',39-40,'X',42-44 <SCH>  
A;/Cross-references: UNIPARC:UPI00001777FD  
A;/Note: evidence for heparan sulfate attachment  
R;/Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.  
FEBS Lett. 349, 109-116, 1994  
A;/Title: The beta-A4 amyloid precursor protein binding to copper.  
A;/Reference number: S46251; MUID:94320627; PMID:7913895  
A;/Contents: annotation; copper binding sites

A;/Note: rat peptides were isolated but not sequenced  
R;/Potempa, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.  
J. Biol. Chem. 266, 8464-8469, 1991  
A;/Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain  
A;/Reference number: A39820; MUID:91217087; PMID:1673681  
A;/Accession: A39820  
A;/Status: preliminary  
A;/Molecule type: protein  
A;/Residues: 18-32 <POT>  
A;/Cross-references: UNIPARC:UPI00001777FE  
A;/Experimental source: brain  
C;/Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is ch  
C;/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;/Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein  
F;625-648/Domain: transmembrane #status predicted <TMM>  
Query Match 68.4%; Score 39; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 620 VGSNKGAI 627  
|||||  
RESULT 13  
JH0773  
Alzheimer's disease amyloid beta protein precursor - African clawed frog  
C;/Species: Xenopus laevis (African clawed frog)  
C;/Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 13-Aug-1999  
C;/Accession: JH0773  
R;/Okado, H.; Okamoto, H.  
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992  
A;/Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental  
A;/Reference number: JH0773; MUID:93129227; PMID:1282805  
A;/Accession: JH0773  
A;/Molecule type: mRNA  
A;/Residues: 1-747 <ORA>  
A;/Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:  
A;/Experimental source: larva  
C;/Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i  
C;/Keywords: alternative splicing; amyloid  
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>  
Query Match 68.4%; Score 39; DB 2; Length 747;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 672 VGSNKGAI 679  
|||||  
RESULT 14  
OPHUA4  
Alzheimer's disease amyloid beta protein precursor [validated] - human  
N;/Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi  
N;/Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular  
protein precursor splice form APP(770)  
C;/Species: Homo sapiens (man)  
C;/Date: 30-Jun-1987 #sequence\_revision 28-Jul-1995 #text\_change 15-Sep-2000  
C;/Accession: S02260; S05194; A32277; A33260; A33486; I39452; I39451; I39453; I59562; A44  
4668; A28583; A29302; A60805; JI0038; S06121; A60355; A59011; A38384; S29076; S38252; S3  
R;/Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey  
Nucleic Acids Res. 17, 517-522, 1989  
A;/Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b  
A;/Reference number: S02260; MUID:89128427; PMID:2783775  
A;/Accession: S02260  
A;/Molecule type: DNA  
A;/Residues: 1-288,'V',365-770 <LEM1>  
A;/Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466  
A;/Note: alternative splice form APP(695)  
R;/Lemaire, H.G.

Submitted to the EMBL Data Library, November 1986

A;Reference number: S05194  
A;Accession: S05194  
A;Molecule type: DNA  
A;Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEMZ>  
A;Cross-references: UNIPARC:UPI000016AEFC; ENBL:X13466; NID:g35598; PIDN:CAA31830.1.; PID:  
A;Note: alternative aplice form APP(695)  
R;La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.  
Biochem. Biophys. Res. Commun. 159, 297-304, 1989  
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote  
A;Reference number: A32277; MUID:89165870; PMID:2538123  
A;Accession: A32277  
A;Molecule type: DNA  
A;Residues: 1-75 <LAF>  
A;Cross-references: UNIPARC:UPI000016AS7D; GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13  
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.  
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989  
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit  
A;Reference number: A33260; MUID:89392030; PMID:2675837  
A;Accession: A33260  
A;Molecule type: DNA  
A;Residues: 656-737 <JOH>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:g178863; PIDN:AAA51768.1.; PID:  
R;Prelti, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.  
Biochem. Biophys. Res. Commun. 170, 301-307, 1990  
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of  
A;Reference number: A35486; MUID:90321244; PMID:2196878  
A;Accession: A35486  
A;Molecule type: DNA  
A;Residues: 672-710 <PREI>  
A;Cross-references: UNIPARC:UPI0000148176  
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 87, 257-263, 1990  
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.  
A;Reference number: I39451; MUID:90236318; PMID:2110105  
A;Accession: I39452  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME  
A;Molecule type: DNA  
A;Residues: 1-770 <YOS1>  
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:g178613; PIDN:AAB59502.1.; PID:  
A;Accession: I39451  
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EME  
A;Molecule type: DNA  
A;Residues: 1-530, 'ONLMVPFAFWKVCGR' <YOS2>  
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:g178608; PIDN:AAB59501.1.; PID:  
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.  
Gene 102, 291-292, 1991  
A;Reference number: A59020; MUID:91340168; PMID:1908403  
A;Contents: annotation; erratum  
A;Note: revised physical map for reference I39451  
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine  
Science 248, 1124-1126, 1990  
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh  
A;Reference number: I39453; MUID:90260663; PMID:2111584  
A;Accession: I39453  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 656-737 <LEV>  
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:g178618; PIDN:AAA51727.1.; PID:  
A;Note: a mutation with 693-Gln is presented  
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.  
Science 254, 97-99, 1991  
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer  
A;Reference number: I59562; MUID:92022553; PMID:1925564  
A;Accession: I59562  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 689-716, 'F', 718-737 <MUR>  
A;Cross-references: UNIPARC:UPI000011F7EA; GB:S57665; NID:g236720; PIDN:AAB19991.1.; PID:  
R;Kamino, K.; Orr, H.T.; Payama, H.; Wijeman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,  
Am. J. Hum. Genet. 51, 998-1014, 1992  
at.

A:Molecule type: mRNA  
A:Residues: 1-344, 'I', 365-770 <P02>  
A:Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA3  
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.  
Nature 331, 530-532, 1988  
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor  
A:Reference number: A38949; MUID:88122641; PMID:2893291  
A:Accession: A38949  
A:Molecule type: mRNA  
A:Residues: 287-367 <KIT>  
A:Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:G  
A:Experimental source: Glioblastoma cell line  
A:Note: alternative splice form APP(770)  
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton  
Brain Res. Mol. Brain Res. 4, 121-131, 1988  
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p  
A:Reference number: A30320  
A:Accession: A30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 284-288, 'V', 365-770 <VIT1>  
A:Cross-references: UNIPARC:UPI0000174094  
A:Accession: B30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 122-288, 'V', 365-770 <VIT2>  
A:Cross-references: UNIPARC:UPI0000174094  
A:Accession: C30320  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 606-770 <VIT3>  
A:Cross-references: UNIPARC:UPI0000174094  
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A  
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988  
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b  
A:Reference number: A31087; MUID:88124954; PMID:2893379  
A:Accession: A31087  
A:Molecule type: mRNA  
Query Match 68.4%; Score 39; DB 1; Length 770;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db 695 VGSNKGAI 702  
RESULT 15  
T29359  
hypothetical protein R05G6.9 - Caenorhabditis elegans  
A:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29359  
R:Murray, J.; Le, T.T.  
submitted to the EMBL Data Library, May 1996  
A:Description: The sequence of C. elegans cosmid R05G6.  
A:Reference number: Z20612  
A:Accession: T29359  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-372 <MUR>  
A:Cross-references: UNIPROT:Q21756; UNIPARC:UPI0000082367; EMBL:U58746; PIDN:AA00626.1;  
A:Experimental source: strain Bristol N2; clone R05G6  
C:Genetics:  
A:Gene: CESP:R05G6.9  
A:Map position: 4  
A:Introns: 80/1; 161/1; 245/1; 286/1  
Query Match 66.7%; Score 38; DB 2; Length 372;  
Best Local Similarity 60.0%; Pred. No. 22;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
Db 139 CVGSKAPLC 148  
RESULT 16  
T22622  
hypothetical protein F54B8.5 - Caenorhabditis elegans  
A:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22622  
R:Barlow, K.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19590  
A:Accession: T22622  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-89 <WIL>  
A:Cross-references: UNIPROT:O45563; UNIPARC:UPI0000075FF1; EMBL:Z93383; PIDN:CAB07627.1;  
A:Experimental source: clone F54B8  
C:Genetics:  
A:Gene: CESP:F54B8.5  
A:Map position: 5  
A:Introns: 48/3  
Query Match 64.9%; Score 37; DB 2; Length 89;  
Best Local Similarity 55.6%; Pred. No. 9.2;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 10  
Db 14 IGLNKGVC 22  
RESULT 17  
H69279  
adenine deaminase (adeC) homolog - Archaeoglobus fulgidus  
A:Species: Archaeoglobus fulgidus  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: H69279  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: H69279  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-556 <KLE>  
A:Cross-references: UNIPROT:O29999; UNIPARC:UPI00000571A6; GB:AE001089; GB:AE000782; NII  
C:Superfamily: adenine deaminase adeC  
Query Match 64.9%; Score 37; DB 2; Length 556;  
Best Local Similarity 60.0%; Pred. No. 50;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CVGSNKGAI 10  
Db 450 CVGVDDGSGIC 459  
RESULT 18  
H69185  
amidophosphoribosyltransferase (EC 2.4.2.14) MTH646 precursor [similarity] - Methanobact  
A:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: H69185  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwnani, N.

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func  
 A;Reference number: A69000; MUID:98037514; PMID:9371463  
 A;Accession: H69185  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-474 <MTH>  
 A;Cross-references: UNIPROT:O26742; UNIPARC:UPI0000132A0A; GB:AE000845; GB:AE000666; NID  
 A;Experimental source: strain Delta H  
 C;Genetics:  
 A;Gene: MTH646  
 A;Start codon: TTG  
 C;Superfamily: amidophosphoribosyltransferase  
 C;Keywords: 4Fe-4S; glycosyltransferase; metalloprotein; pentosyltransferase  
 F;1-10/Domain: propeptide #status predicted <PRO>  
 F;11-474/Product: amidophosphoribosyltransferase #status predicted <MAT>  
 F;11/Active site: Cys #status predicted  
 F;250,396,447,450/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
 Query Match 63.2%; Score 36; DB 2; Length 474;  
 Best Local Similarity 50.0%; Pred. No. 66; Mismatches 3; Indels 0; Gaps 0;  
 Matches 5; Conservative 2;  
 QY 1 CVGSNKGALC 10  
 |: :|||:  
 Db 438 CIGIKKGFLC 447  
 RESULT 19  
 A69493  
 cysteine proteinase homolog - Archaeoglobus fulgidus  
 C;Species: Archaeoglobus fulgidus  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: A69493  
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woese, C.R.; Venter, J.C.  
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae  
 A;Reference number: A69250; MUID:98049343; PMID:9389475  
 A;Accession: A69493  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-1088 <KJL>  
 A;Cross-references: UNIPROT:O28333; UNIPARC:UPI0000056B2A; GB:AE000969; GB:AE000782; NID  
 Query Match 63.2%; Score 36; DB 2; Length 1088;  
 Best Local Similarity 50.0%; Pred. No. 14e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 5; Conservative 3;  
 QY 1 CVGSNKGALC 10  
 |: :|||:  
 Db 123 CISTSKGDLIC 132  
 RESULT 20  
 T18688  
 hypothetical protein B0272.5b - Caenorhabditis elegans (fragment)  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T18688  
 R;Sulston, J.  
 submitted to the EMBL Data Library, October 1994  
 A;Reference number: Z19006  
 A;Accession: T18688  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1555 <WIL>  
 A;Cross-references: UNIPROT:Q8IG47; UNIPARC:UPI000017A08B; EMBL:Z46240; NID:g5559408; PID  
 A;Experimental source: clone B0272

C;Genetics:  
 A;Gene: CBSP:B0272.5b  
 A;Map position: X

Query Match 63.2%; Score 36; DB 2; Length 1555;  
 Best Local Similarity 60.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGALC 10  
 |: :|||:  
 Db 1332 CMGPKNPAYC 1341

RESULT 21  
 G89608

protein B0272.5 [imported] - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C;Accession: G89608  
 R;anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo  
 A;Reference number: A75000; MUID:99069613; PMID:9851916  
 A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.el  
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an  
 A;Accession: G89608  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1973 <STO>  
 A;Cross-references: UNIPROT:Q8IG48; UNIPARC:UPI000017A08A; GB:chr\_X; PIDN:CAA86313.1; P  
 C;Genetics:  
 A;Gene: B0272.5  
 A;Map position: X

Query Match 63.2%; Score 36; DB 2; Length 1973;  
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGALC 10  
 |: :|||:  
 Db 1750 CMGPKNPAYC 1759

RESULT 22

T18686  
 hypothetical protein B0272.5a - Caenorhabditis elegans (fragment)  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T18686  
 R;Sulston, J.  
 submitted to the EMBL Data Library, October 1994  
 A;Reference number: Z19006  
 A;Accession: T18686  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1973 <WIL>  
 A;Cross-references: UNIPROT:Q8IG48; UNIPARC:UPI000017A08A; EMBL:Z46240; NID:g5559408; PI  
 A;Experimental source: clone B0272  
 C;Genetics:  
 A;Gene: CBSP:B0272.5a  
 A;Map position: X

Query Match 63.2%; Score 36; DB 2; Length 1973;  
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGALC 10  
 |: :|||:  
 Db 1750 CMGPKNPAYC 1759

RESULT 23  
 P95294

probable LysR-type regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: F95294  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: F95294  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-299 <KUR>  
A:Cross-references: UNIPROT:Q930D6; UNIPARC:UPI00000C8030; GB:AE006469; PIDN:AAK64920.1;  
A:Experimental source: strain 1021, magaplasmid pSymA  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaullt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: SMA0498  
A:Genome: plasmid

Query Match 61.4%; Score 35; DB 2; Length 299;  
Best Local Similarity 75.0%; Pred. No. 66;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
:|||||  
Db 270 IGTNKGAI 277

RESULT 24  
A56175  
adhesive plaque protein Mgf2 precursor - Mediterranean mussel  
C:Species: Mytilus galloprovincialis (Mediterranean mussel)  
C:Date: 27-Apr-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: A56175  
R:Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.  
J. Biol. Chem. 270, 6698-6701, 1995  
A:Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor  
A:Reference number: A56175; MUID:95204464; PMID:7896812  
A:Accession: A56175  
A:Molecule type: mRNA  
A:Residues: 1-473 <INO>  
A:Cross-references: UNIPROT:Q25464; UNIPARC:UPI000012AB7B; GB:D43794; NID:9602767; PIDN:  
C:Keywords: duplication  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:387-419/Domain: EGF homology <EGF1>  
F:429-460/Domain: EGF homology <EGF>  
F:23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 61.4%; Score 35; DB 2; Length 473;  
Best Local Similarity 60.0%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
|||||  
Db 330 CVGGYKGPTC 339

RESULT 25  
H69980  
single-strand DNA-specific exonuclease homolog yrvE - Bacillus subtilis  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: H69980  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc  
A.; Ehrlich, S.D.; Emerson, P.T.; Encian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Hosono, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Mausel  
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieser, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: H69980  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-786 <KUN>  
A:Cross-references: UNIPROT:O32044; UNIPARC:UPI0000060827; GB:Z99118; GB:AL009126; NID:9  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yrvE

Query Match 61.4%; Score 35; DB 2; Length 786;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 9  
|||||  
Db 518 CVGFNKGEL 526

RESULT 26  
A38725  
transferrin - sheep (fragments)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 20-Sep-1991 #sequence\_revision 20-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: A38725  
R:Tsu, G.F.; Achen, M.G.; Aldred, A.R.; Southwell, B.R.; Schreiber, G.  
J. Biol. Chem. 266, 6201-6208, 1991  
A:Title: The distribution of cerebral expression of the transferrin gene is species spec  
A:Reference number: A38725; MUID:91177867; PMID:1848850  
A:Accession: A38725  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-87 <TUA>  
A:Cross-references: UNIPROT:Q99149; UNIPARC:UPI0000088AFA; GB:M64692  
C:Superfamily: transferrin; transferrin repeat homology  
C:Keywords: duplication

Query Match 59.6%; Score 34; DB 2; Length 87;  
Best Local Similarity 62.5%; Pred. No. 32;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 8  
|||||  
Db 64 CIGSEKGS 71

RESULT 27  
TI9573  
hypothetical protein C29F7.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: TI9573  
R:McMurray, A.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19144  
A:Accession: TI9573  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-191 <WIL>

A;Cross-references: UNIPROT:O17622; UNIPARC:UPI000007E454; EMBL:Z92827; PIDN:CA807328.1;  
A;Experimental source: clone C29F7  
C;Genetics:  
A;Gene: CBSP:C29F7.3  
A;Map position: X  
A;Introns: 24/3; 73/3; 176/3  
C;Superfamily: adenylate kinase

Query Match 59.6%; Score 34; DB 2; Length 191;  
Best Local Similarity 75.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSNKGAIC 10  
|||  
DB 12 GSGKGTIC 19

RESULT 28  
T22036  
hypothetical protein F40F8.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22036  
R;MacDougall, R.  
submitted to the EMBL Data Library, February 1996  
A;Reference number: Z19505  
A;Accession: T22036  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-191 <WIL>  
A;Cross-references: UNIPROT:Q20230; UNIPARC:UPI000007A508; EMBL:Z69302; PIDN:CAA93264.1;  
A;Experimental source: clone F40F8  
C;Genetics:  
A;Gene: CBSP:F40F8.1  
A;Map position: 2;  
A;Introns: 24/3  
C;Superfamily: adenylate kinase

Query Match 59.6%; Score 34; DB 2; Length 191;  
Best Local Similarity 75.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GSNKGAIC 10  
|||  
DB 12 GSGKGTIC 19

RESULT 29  
E71812  
transaldolase - Helicobacter pylori (strain J99)  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: E71812  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Malls, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: E71812  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-316 <ARN>  
A;Cross-references: UNIPROT:Q9ZJC5; UNIPARC:UPI00001368B0; GB:AE001561; GB:AE001439; NID  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: tal  
C;Superfamily: human transaldolase

Query Match 59.6%; Score 34; DB 2; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKGAIC 10  
|||||  
DB 25 NKGAIC 30

## RESULT 30

G64706

transaldolase - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004

C;Accession: G64706

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185

A;Accession: G64706

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residue type: DNA

A;Molecules: 1-316 &lt;TOM&gt;

A;Cross-references: UNIPROT:P56108; UNIPARC:UPI00001368B1; GB:AE000648; GB:AE000511; NID

C;Superfamily: human transaldolase

Query Match 59.6%; Score 34; DB 2; Length 316;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKGAIC 10

|||||

DB 25 NKGAIC 30

## RESULT 31

T22998

hypothetical protein F59D12.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T22998

R;Illoyd, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19649

A;Accession: T22998

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-356 &lt;WIL&gt;

A;Cross-references: UNIPROT:Q9XUV6; UNIPARC:UPI0000081920; EMBL:Z81558; PIDN:CA804541.1; NID

A;Experimental source: clone F59D12

C;Genetics:

A;Gene: CBSP:F59D12.3

A;Map position: X

A;Introns: 40/1; 111/3; 158/2; 202/2; 252/2; 306/1

Query Match

Best Local Similarity 59.6%; Score 34; DB 2; Length 356;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CVGSKNGAIC 10

|||||

DB 211 CVGCKNDMVC 220

## RESULT 32

T51506

hypothetical protein F5E19.80 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004

C;Accession: T51506

R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asanizu, E.; Kotani, H.; Tabata, S.; Me-

submitted to the Protein Sequence Database, August 2000

A;Reference number: Z25394

A;Accession: T51506

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-426 <SAT>  
A:Cross-references: UNIPROT:Q9LFE3; UNIPARC:UPI00000A18E2; EMBL:AL391147  
A:Experimental source: cultivar Columbia; BAC clone F5E19  
C:Genetics:  
A:Map position: 5  
A:Introns: 48/1; 247/3  
A:Note: F5E19\_80  
C:Superfamily: Arabidopsis amino acid transport protein I

Query Match 59.6%; Score 34; DB 2; Length 426;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CVGSNKGGAIC 10  
||| ||| |  
Db 6 CVEENKGCBC 15

RESULT 33  
G70116  
histidine-tRNA ligase (EC 6.1.1.21) hisS - Lyme disease spirochete  
N:Alternate names: histidyl-tRNA synthetase  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: G70116  
R:Fraser, C.M.; Cailjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943; PMID:9403685  
A:Accession: G70116  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-457 <KLZ>  
A:Cross-references: UNIPROT:O51160; UNIPARC:UPI0000057372; GB:AE001125; GB:AE000783; NID  
A:Experimental source: strain B31  
C:Superfamily: histidyl-tRNA synthetase; histidine-tRNA ligase homology  
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis  
F:8-418/Domain: histidine-tRNA ligase homology <HTL>

Query Match 59.6%; Score 34; DB 1; Length 457;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GSNKGAIC 10  
||| ||| |  
Db 290 GSNMGSGVC 297

RESULT 34  
T45816  
hypothetical protein F2809.230 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T45816  
R:Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.  
submitted to the Protein Sequence Database, January 2000  
A:Reference number: Z23014  
A:Status: preliminary  
A:Accession: T45816  
A:Molecule type: DNA  
A:Residues: 1-470 <BEN>  
A:Cross-references: UNIPROT:Q9M2K9; UNIPARC:UPI000009D548; EMBL:AL137080  
A:Experimental source: cultivar Columbia; BAC clone F2809  
C:Genetics:  
A:Map position: 3  
A:Introns: 33/1; 59/1  
A:Note: F2809.230  
C:Superfamily: Arabidopsis thaliana hypothetical protein F2809.230

Query Match 59.6%; Score 34; DB 2; Length 470;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGGAIC 10  
||| ||| |  
Db 53 CSGTSGNGTIC 62

RESULT 35  
S76211  
hypothetical protein slr0442 - Synecocystis sp. (strain PCC 6803)  
C:Species: Synecocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76211  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis  
s.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76211  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-611 <KAN>  
A:Cross-references: UNIPROT:P74375; UNIPARC:UPI00000C0E6B; EMBL:D90914; GB:AB001339; NID  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 59.6%; Score 34; DB 2; Length 611;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VGSNKGGAIC 10  
||| ||| |  
Db 114 VSSNSGSGIC 122

RESULT 36  
T20839  
hypothetical protein F13E9.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20839  
R:McMurray, A.  
submitted to the EMBL Data Library, February 1996  
A:Reference number: Z19332  
A:Accession: T20839  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-615 <WIL>  
A:Cross-references: UNIPROT:Q19406; UNIPARC:UPI0000078E80; EMBL:Z69383; PIDN:CAA93404.1;  
A:Experimental source: clone F13E9  
C:Genetics:  
A:Gene: CESP:F13E9.8  
A:Map position: 4  
A:Introns: 58/3; 181/1; 298/3; 360/3; 402/3; 514/2; 537/3

Query Match 59.6%; Score 34; DB 2; Length 615;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGGA 8  
||| ||| |  
Db 576 CVGKKKGA 583

RESULT 37  
T19346  
hypothetical protein C17D12.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999



C:Accession: T19346  
 R:White, S.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19112  
 A:Accession: T19346  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-640 <WIL>  
 A:Cross-references: UNIPARC:UPI000017B793; EMBL:Z81473; PIDN:CAB03894.1; GSPDB:GN000019;  
 A:Experimental source: clone C17D12  
 C:Genetics:  
 A:Gene: CESP-C17D12.6  
 A:Map position: 1  
 A:Introns: 16/1; 49/3; 75/2; 111/2; 207/3; 232/3; 255/1; 290/2; 337/1; 447/3; 501/2; 560/2

Query Match 59.6%; Score 34; DB 2; Length 640;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 9  
 |:| |||||  
 Db 181 CLGRGKGAI 189

RESULT 38  
 B71409  
 hypothetical protein - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cross)  
 A:Variety: Columbia  
 C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
 C:Accession: B71409  
 R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
 P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giel  
 avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
 Nature 391, 485-486, 1998  
 A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
 erhoft, A.; Moores, J.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans  
 C.; Chalwatzis, N.  
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
 A:Reference number: A71400; MUID:98121113; PMID:9461215  
 A:Accession: B71409  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-644 <BEV>  
 A:Cross-references: UNIPROT:O23321; UNIPARC:UPI00000AA0C0; GB:Z97336; NID:g2244788; PID:  
 C:Genetics:  
 A:Map position: 4COP9-4G3845

Query Match 59.6%; Score 34; DB 2; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVGSNK 6  
 |:| |||||  
 Db 505 CVGSNK 510

RESULT 39  
 A42287  
 phosphoprotein phosphatase (EC 3.1.3.16) rdgC - fruit fly (Drosophila melanogaster)  
 N:Alternate names: retinal degeneration protein C  
 C:Species: Drosophila melanogaster  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 12-Jul-2004  
 C:Accession: A42287; S27811  
 R:Steele, F.R.; Washburn, T.; Rieger, R.; O'Tousa, J.E.  
 Cell 69, 669-676, 1992  
 A:Title: Drosophila retinal degeneration C (rdgC) encodes a novel serine/threonine prote  
 A:Reference number: A42287; MUID:92266398; PMID:1316807  
 A:Accession: A42287  
 A:Molecule type: DNA  
 A:Residues: 1-661 <STE>  
 A:Cross-references: UNIPROT:P40421; UNIPARC:UPI00000072BA; EMBL:M89628; NID:g158237; PID  
 A:Note: sequence extracted from NCBI backbone (NCBIN:103017, NCBIN:103023, NCBIN:103028,

, NCBIN:103104, NCBIP:103001)  
 C:Genetics:  
 A:Gene: rdgC  
 A:Cross-references: FlyBase:FBgn0004366  
 A:Introns: 5/1; 47/3; 74/3; 116/3; 172/3; 240/3; 290/3; 312/3; 374/3; 510/3; 544/1  
 C:Function:  
 A:Description: catalyzes the hydrolytic dephosphorylation of protein-phosphoserine and  
 A:Note: prevents light-induced retinal degeneration  
 C:Superfamily: serine/threonine protein phosphatase with EF-hands; calmodulin repeat hom  
 C:Keywords: calcium binding; EF hand; iron; metalloprotein; nucleus; phosphoric monoest  
 F:120-401/Domain: phosphoprotein phosphatase homology <PPP>  
 F:152-221/Domain: phosphoserase core homology <PEP>  
 F:526-558/Domain: calmodulin repeat homology <EF1>  
 F:566-598/Domain: calmodulin repeat homology <EF2>  
 F:158,160,187/Binding site: iron (Asp, His, Asp) #status predicted  
 F:187,219,271,360/Binding site: zinc (Asp, Asn, His, His) #status predicted  
 F:190,220,384/Active site: Asp, His, Tyr #status predicted  
 F:191,333/Binding site: substrate phosphate (Arg) #status predicted

Query Match 59.6%; Score 34; DB 1; Length 661;  
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 8  
 |:| |||||  
 Db 387 IGSNKGAI 393

RESULT 40  
 T42754  
 hypothetical protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C:Accession: T42754  
 R:Singston, A.; Mercer, K.B.; L'Hernault, S.W.  
 Cell 93, 71-79, 1998  
 A:Title: The Caenorhabditis elegans spe-9 gene encodes a sperm transmembrane protein th  
 A:Reference number: Z22261; MUID:98206469; PMID:9546393  
 A:Accession: T42754  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-661 <SIN>  
 A:Cross-references: UNIPROT:Q9TVY6; UNIPARC:UPI000008233E; EMBL:AF049327; NID:g3015634;  
 C:Genetics:  
 A:Gene: spe-9

Query Match 59.6%; Score 34; DB 2; Length 661;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 9  
 |:| |||||  
 Db 181 CLGRGKGAI 189

Search completed: January 28, 2006, 00:59:16  
 Job time : 20 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 00:53:21 ; Search time 70 Seconds  
(without alignments)  
100.790 Million cell updates/sec

Title: US-09-018-194A-4

Perfect score: 57

Sequence: 1 CVGSNKGARC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

UniProt\_05.80.\*  
1: uniprot\_spot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	71.9	76	2	Q9LRD8 BRACM
2	40	70.2	284	2	Q9PD24 XYLFA
3	39	68.4	33	2	Q9UC33 HUMAN
4	39	68.4	42	2	Q5GJ06 GRAGR
5	39	68.4	42	2	Q5GJ07 TURTR
6	39	68.4	42	2	Q7M088 CAVPO
7	39	68.4	49	2	Q97917 BOVIN
8	39	68.4	52	2	Q8WZ99 HUMAN
9	39	68.4	57	1	A4 UR5MA
10	39	68.4	58	1	A4 CANFA
11	39	68.4	58	1	A4 RABIT
12	39	68.4	58	1	A4 SHEEP
13	39	68.4	59	1	A4 BOVIN
14	39	68.4	79	2	Q35463 CRIGR
15	39	68.4	80	2	Q2BP85 CONAE
16	39	68.4	113	2	Q8BP85 CHESE
17	39	68.4	218	2	Q8BPV5 MOUSE
18	39	68.4	310	2	Q5S1V7 SACOF
19	39	68.4	384	2	Q8BPC7 MOUSE
20	39	68.4	386	2	Q572X2 9TRYP
21	39	68.4	393	2	Q701K1 ANOGA
22	39	68.4	513	2	Q9V8N4 DROME
23	39	68.4	534	2	Q93296 CHICK
24	39	68.4	569	2	Q9PVL1 CHICK
25	39	68.4	617	2	Q86BF1 DROME
26	39	68.4	620	2	Q81H99 DROME
27	39	68.4	693	2	Q9S8G0 XENLA
28	39	68.4	695	2	Q5R477 PONPY
29	39	68.4	695	2	Q6RH29 CANFA
30	39	68.4	695	2	Q56JK3 CANFA
31	39	68.4	695	2	Q6GR78 MOUSE

32	39	68.4	695	2	Q9DGJ8 CHICK	Q9dgj8 gallus gall
33	39	68.4	695	2	Q98SF9 XENLA	Q98sf9 xenopus lae
34	39	68.4	695	2	Q7ZXQ0 XENLA	Q7zxq0 xenopus lae
35	39	68.4	699	2	O57394 NARJA	O57394 narke japon
36	39	68.4	714	2	O56JK4 CANFA	O56jk4 canis famli
37	39	68.4	733	2	Q6PQ5 RAT	Q6pq5 rattus norv
38	39	68.4	737	1	A4 FUGRU	Q93279 fugu rubrip
39	39	68.4	747	2	Q91963 9PIPI	Q91963 xenopus. ap
40	39	68.4	749	2	O56JK2 STXCO	O56jk2 stenella co
41	39	68.4	749	2	Q6NRR1 XENLA	Q6nr1 xenopus lae
42	39	68.4	750	2	Q6DJ6 XENTR	Q6dj6 xenopus tro
43	39	68.4	751	1	A4 SAISC	Q95241 s amyloid b
44	39	68.4	751	2	Q6GSCO HUMAN	Q6gsc0 homo sapien
45	39	68.4	751	2	Q6RH28 CANFA	Q6rh28 canis famli
46	39	68.4	751	2	O56JK5 CANFA	O56jk5 canis famli
47	39	68.4	751	2	Q4R4R8 MACFA	O4r4r8 macaca fasc
48	39	68.4	751	2	Q9DGJ7 CHICK	Q9dgj7 gallus gall
49	39	68.4	754	2	Q4RY33 TETNG	Q4ry33 tetraodon n
50	39	68.4	759	2	Q4S0J4 TETNG	Q4s0j4 tetraodon n
51	39	68.4	770	1	A4 CAVPO	Q60495 c amyloid b
52	39	68.4	770	1	A4 HUMAN	P05067 h amyloid b
53	39	68.4	770	1	A4 MACFA	P53601 m amyloid b
54	39	68.4	770	1	A4 MOUSE	P12023 m amyloid b
55	39	68.4	770	1	A4 PANTR	P51880 p amyloid b
56	39	68.4	770	1	A4 PIG	P79307 s amyloid b
57	39	68.4	770	1	A4 RAT	P08592 r amyloid b
58	39	68.4	770	2	Q6RH30 CANFA	Q6rh30 canis famli
59	39	68.4	770	2	O56JK6 CANFA	O56jk6 canis famli
60	39	68.4	770	2	Q53T3 MOUSE	Q53t3 mus musculu
61	39	68.4	770	2	Q547B7 RAT	Q547b7 rattus norv
62	39	68.4	780	1	A4 TETFL	Q73683 tetraodon f
63	39	68.4	1268	2	O5CVS0 CRYPV	O5cvs0 cryptospori
64	39	68.4	1268	2	O5CJ08 CRYHO	O5cj08 cryptospori
65	39	68.4	1269	2	O57WX5 9TRYP	O57wx5 trypanosoma
66	39	68.4	1732	2	Q4LDF5 CHICK	Q4lfd5 gallus gall
67	38.5	67.5	238	2	Q5L956 BACFN	Q5l956 bacteroides
68	38	66.7	274	2	Q8FED1 ECOLF	Q8fed1 escherichia
69	38	66.7	374	2	Q61T55 CAEBR	Q61t55 caenorhabdi
70	38	66.7	378	2	Q21756 CAEEL	Q21756 caenorhabdi
71	38	66.7	808	2	O5KYT3 GEOKA	Q5kyt3 geobacillus
72	38	66.7	919	2	Q8V0A2 TETNG	Q8v0a2 tetraodon n
73	38	66.7	1136	2	Q8V6X1 9VIRU	Q8v6x1 iris yellow
74	37.5	65.8	84	2	Q7QVW0 GIALA	Q7qvw0 giardia lam
75	37	64.9	84	2	O6ICE1 DROME	O6ice1 drosophila
76	37	64.9	89	2	O45563 CAEEL	O45563 caenorhabdi
77	37	64.9	313	2	Q7XM81 ORYSA	Q7xm81 oryza sativ
78	37	64.9	322	2	Q62MV3 BURMA	Q62mv3 burkholderi
79	37	64.9	322	2	Q63YT2 BURPS	Q63yt2 burkholderi
80	37	64.9	384	2	P96478 STRPN	P96478 streptococc
81	37	64.9	507	2	Q86A93 DICDI	Q86a93 dictyosteli
82	37	64.9	556	1	ADEC ARCFU	O29999 archaeoglob
83	37	64.9	560	2	O61085 DICDI	O61085 dictyosteli
84	37	64.9	560	2	Q555U1 DICDI	Q555u1 dictyosteli
85	37	64.9	574	2	Q4REA6 TETNG	Q4rea6 tetraodon n
86	37	64.9	604	2	Q7F8U2 ORYSA	Q7f8u2 oryza sativ
87	37	64.9	611	2	O69QR7 ORYSA	Q69qr7 oryza sativ
88	37	64.9	779	2	Q7Q811 ANOGA	Q7q811 anopheles g
89	37	64.9	871	2	Q81D27 PLAF7	Q81d27 plasmodium
90	37	64.9	936	2	Q6FJ20 CANGA	Q6fj20 candida gla
91	37	64.9	1149	2	Q811U0 MOUSE	Q811u0 mus musculu
92	37	64.9	1223	2	O5ZAP0 ORYSA	O5zap0 oryza sativ
93	37	64.9	1361	2	Q9NGV2 DROME	Q9ngv2 drosophila
94	37	64.9	1361	2	Q9V7I4 DROME	Q9v7i4 drosophila
95	37	64.9	2203	2	Q812C4 PLAF7	Q812c4 plasmodium
96	37	64.9	2646	2	Q81220 PLAF7	Q81220 plasmodium
97	37	64.9	3525	2	Q815W5 PLAF7	Q815w5 plasmodium
98	37	64.9	4699	2	Q9V383 DROME	Q9v383 drosophila
99	36	63.2	153	2	Q7UHX3 ROBA	Q7uhx3 rhodopirell
100	36	63.2	239	2	Q8UUI7 BRARE	Q8uui7 brachydanio

ALIGNMENTS

```

RESULT 1
Q9LRD8 BRACM
ID Q9LRD8_BRACM PRELIMINARY; PRT; 76 AA.
AC Q9LRD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S locus protein 11-34 (fragment).
GN Name=Sp11-34;
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S34;
RX MEDLINE=20273842; PubMed=10812061; DOI=10.1016/S0014-5793(00)01514-3;
RA Watanabe M., Ito A., Takada Y., Ninomiya C., Kakizaki T., Takahata Y.,
RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satta Y., Shiba H.,
RA Takayama S., Isogai A.;
RT "Highly divergent sequences of the pollen self-incompatibility (S)
RT gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";
RL FEBS Lett. 473:139-144 (2000).
DR EMBL; AB039758; BAA96396.1; -; mRNA.
DR InterPro; IPR010882; SCRL.
DR Pfam; PF06876; SCRL; 1.
FT NON TER 1
SQ SEQUENCE 76 AA; 8730 MW; 4018830CF39600A6 CRC64;

Query Match 71.9%; Score 41; DB 2; Length 76;
Best Local Similarity 70.0%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVGSNKGAI 10
||| | |
Db 56 CVGSRKHLC 65

RESULT 2
Q9PD24 XYLFA
ID Q9PD24_XYLFA PRELIMINARY; PRT; 284 AA.
AC Q9PD24;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phage-related protein.
GN OrderedLocusNames=Xf1555;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reilnach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Ferreira E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

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RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto R.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi W.F., Truffi D., Tsai S.M., Tettore A.L.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore M.H.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159 (2000).
DR EMBL; AE003985; AAF84364.1; -; Genomic_DNA.
DR PIR; P82666; P82666.
DR HSSP; P03700; IAE9.
DR GO; GO:0015074; P:DNA integration; IEA.
KW Complete proteome.
SQ SEQUENCE 284 AA; 32141 MW; 2D4971341AF3F048 CRC64;

Query Match 70.2%; Score 40; DB 2; Length 284;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVGSNKGAI 10
||| | |
Db 248 CVGDDGALC 257

RESULT 3
Q9UC33 HUMAN
ID Q9UC33_HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Beta-amyloid peptide (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327 (1992).
DR HSSP; Q16019; IBA4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMVLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DFE2F4167ABD0 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9
||| | |
Db 24 VGSNKGAI 31

RESULT 4
Q56J06 GRAGR
ID Q56J06_GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56J06;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

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DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -, mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 24 VGSNKGAI 31

RESULT 5
Q56JJ7 TURTR
ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.
AC Q56JJ7;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Turlops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -, mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 24 VGSNKGAI 31

RESULT 6
Q7M088 CAVPO
ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
RN [1]
RP PROTEIN SEQUENCE.
RT MEDLINE=93290653; PubMed=7685598;

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RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance p receptors";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR PIR; P0512; P0512.
DR HSP; Q16019; I1YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 24 VGSNKGAI 31

RESULT 7
O97917 BOVIN
ID O97917 BOVIN PRELIMINARY; PRT; 49 AA.
AC O97917;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20063685; PubMed=10594237; DOI=10.1007/s003359901180;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RT level of polymorphism in both intron and exon.";
RL Mamm. Genome 10:1142-1145(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Miller R.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133033; CAB38017.1; -, Genomic_DNA.
DR HSP; Q16019; I1YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 68.4%; Score 39; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 7 VGSNKGAI 14

RESULT 8
Q8WZ99 HUMAN
ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.

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AC Q8WZ99;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
EX PubMed:15201367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
RA Nimomiya H., Saito T.C., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RT probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;

Query Match 68.4%; Score 39; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 9
A4 URSMA
ID A4 URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
OC Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; X56128; CAA39593.1; -; mRNA.
DR PIR; B60045; B60045.
DR HSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 EXTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1
FT CHAIN 6 >57 Soluble APP-beta (By similarity).
FT CHAIN 6 >47 CTF-alpha (By similarity).
FT CHAIN 6 >45 Beta-amyloid protein 42 (By similarity).
FT CHAIN 46 >57 Beta-amyloid protein 40 (By similarity).
FT CHAIN 48 >57 Gamma-CTF(59) (By similarity).
FT TRANSMEM 34 >57 Gamma-CTF(57) (By similarity).
FT NON_TER 1 Extracellular (Potential).
FT NON_TER 57 Potential.
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 68.4%; Score 39; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 29 VGSNKGAI 36

RESULT 10
A4 CANFA
ID A4 CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
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CC removed.
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DR EMBL; X56125; CAA39590.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; ENSCARG000008557; Canis familiaris.
DR Ensemble; IPR001255; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR Amyloid; Transmembrane.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >58 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8459D488A2E12DFA CRC64;

Query Match 68.4%; Score 39; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
DB 30 VGSNKGAI 37

RESULT 11
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
DR Amyloid; Transmembrane.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D98E8BA82D CRC64;

Query Match 68.4%; Score 39; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
DB 29 VGSNKGAI 36

RESULT 12
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
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DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF (59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF (57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 68.4%; Score 39; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 29 VGSNKGAI 36

RESULT 13
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF (59) (Gamma-secreta
DE C-terminal fragment 59); Gamma-CTF (57) (Gamma-secreta C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92010709; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X56124; CAA39589.1; -; mRNA.
DR EMBL; X56126; CAA39591.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR InterPro; IPR008155; A4_APP.

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DR InterPro; IPR001255; Beta-APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >59 CTF-alpha (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >59 Gamma-CTF (59) (By similarity).
FT CHAIN 49 >59 Gamma-CTF (57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 68.4%; Score 39; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 30 VGSNKGAI 37

RESULT 14
Q35463 CRIGR PRELIMINARY; PRT; 79 AA.
ID Q35463_CRIGR PRELIMINARY; PRT; 79 AA.
AC Q35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Name=beta APP;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 44 VGSNKGAI 51

RESULT 15
Q9BP85 CONAE PRELIMINARY; PRT; 80 AA.
ID Q9BP85_CONAE PRELIMINARY; PRT; 80 AA.
AC Q9BP85;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Conotoxin scaffold VI/VII.  
 OS Conus arenatus (Sand-dusted cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89451;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21105969; PubMed=11158371;  
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,  
 RA Fainzilber M.;  
 RT "Mechanisms for evolving hypervariability: the case of conopeptides.";  
 RL Mol. Biol. Evol. 18:120-131(2001).  
 DR EMBL; AF215053; AAG60481.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.  
 DR GO; GO:0009405; P:pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR Pfam; PF02950; Conotoxin; 1.  
 SQ SEQUENCE 80 AA; 8724 MW; 3A516A7280D9872D CRC64;

Query Match 68.4%; Score 39; DB 2; Length 80;  
 Best Local Similarity 60.0%; Pred. No. 14;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSKNGAIC 10 PRT; 113 AA.  
 ||||| |:  
 Db 68 CVGSRFGGLC 77

## RESULT 16

Q8JH58 CHESE PRELIMINARY; PRT; 113 AA.  
 AC Q8JH58;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Amyloid beta protein (Fragment).  
 OS Chelydra serpentina serpentina (common snapping turtle).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Testudines; Cryptodira; Testudinoida; Chelydridae; Chelydra.  
 OX NCBI\_TaxID=134619;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21876906; PubMed=11882478;  
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;  
 RT "Octylphenol (OP) alters the expression of members of the amyloid  
 RT protein family in the hypothalamus of the snapping turtle, Chelydra  
 RL serpentina serpentina.";  
 RL Environ. Health Perspect. 110:269-275(2002).  
 DR HSP; Q16019; IYT.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR008155; A4 APP.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOID4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PROSITE; PS00320; A4 INTRA; 1.  
 FT NON TER 1  
 SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNGKAI 9  
 |||||  
 Db 38 VGSNGKAI 45

RESULT 17  
 Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.  
 AC Q8BPV5;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched  
 DE library, clone:D430025B14 product:amyloid beta (A4) protein, full  
 DE insert sequence. (Fragment).  
 GN Name-App;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Lung;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Lung;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata K., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Lung;  
 RC The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Lung;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RX STRAIN=C57BL/6J; TISSUE=Lung;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka S., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (KISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer."; [6]  
 RL Genome Res. 10:1757-1771(2000).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=Lung;  
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK052448; BAC34997.1; -; mRNA.  
 DR HSP; P08592; 1NMJ.  
 DR MGI; MGI:88059; App.  
 DR GO; GO:0016021; C:integral to membrane; IDA.  
 DR GO; GO:0016020; C:membrane; TAS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0030198; F:extracellular matrix organization and bioge. . .; IGI.  
 DR InterPro; IPR008155; A4 APP.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 218;  
 Best Local Similarity 100.0%; Pred. No. 40;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 Db 143 VGSNKGAI 150  
 |||||  
 |||||

RESULT 18  
 Q5S1V7 SACOF  
 ID Q5S1V7\_SACOF PRELIMINARY; PRT; 310 AA.  
 AC Q5S1V7  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE 1-aminocyclopropane-1-carboxylate synthase (Fragment).  
 GN Name=acs3;  
 OS Saccharum officinarum (Sugarcane).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Saccharum;  
 OC Saccharum officinarum complex.  
 OX NCBI\_TaxID=4547;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stauber F., Suzuki R., Tonita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."; [3]  
 RL Nature 409:695-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA The FANTOM Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";

DR InterPro; IPR004839; Aminotrans I/II.  
 DR InterPro; IPR004838; NHtransf\_1\_BS.  
 DR Pfam; PF00155; Aminotran\_1\_2; 1.  
 DR PRINTS; PR00753; ACCSYNTHASE.  
 DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 KW Pyridoxal phosphate.  
 FT NON\_TER 1  
 FT NON\_TER 310  
 SQ SEQUENCE 310 AA; 33852 MW; 09C8ACDA300286FA CRC64;

Query Match 68.4%; Score 39; DB 2; Length 310;  
 Best Local Similarity 60.0%; Pred. No. 58;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10  
 Db 254 CLGSNAGLFC 263  
 |||||  
 |||||

RESULT 19  
 QB8PC7 MOUSE  
 ID QB8PC7\_MOUSE PRELIMINARY; PRT; 384 AA.  
 AC QB8PC7;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched  
 DE library, clone:483342109 product:amyloid beta (A4) protein, full  
 DE insert sequence. (Fragment).  
 GN Name=App;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning."; [2]  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stauber F., Suzuki R., Tonita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."; [3]  
 RL Nature 409:695-690(2001).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA The FANTOM Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Iogawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK076506; BAC36369.1; -, mRNA.  
 DR HSSP; P08592; INMJ.  
 DR SMR; QBPC7; 74-183.  
 DR MGI; MGI:88059; App.  
 DR GO; GO:0016021; C:membrane; TAS.  
 DR GO; GO:0016020; C:membrane binding; IPI.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IGI.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR001255; Beta\_APP.  
 DR Pfam; PF03494; Beta\_APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8A5683173 CRC64;  
 Query Match 68.4%; Score 39; DB 2; Length 384;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9 PRT; 386 AA.  
 Db 309 VGSNKGAI 316  
 RESULT 20  
 ID Q57ZX2\_9TRY PRELIMINARY; PRT; 386 AA.  
 AC Q57ZX2\_9  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Phosphoribosylpyrophosphate synthetase, putative (EC 2.7.6.1).

GN ORFNames=Tb927.5.2960;  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5691;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUTat10.1;  
 RA Ghedin E., Blandin G., Bartholomeu D., Caler E., Haas B., Hannick L.,  
 RA Shallom J., Hou L., Djikeng A., Feldblyum T., Hostetler J.,  
 RA Johnson J., Jones K., Koo H.L., Larkin C., Pai G., Peterson J.,  
 RA Khalak H.G., Salzberg S., Simpson A.J., Tallon L., Van Aken S.,  
 RA Wanless D., White O., Wortman J., Fraser C.M., El-Sayed N.M.A.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUTat10.1;  
 RA El-Sayed N.M., Khalak H., Adams M.D.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=GUTat10.1;  
 RA Haas B., Blandin G., El-Sayed N.;  
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC104488; AAX79353.1; -, Genomic DNA.  
 DR GO; GO:0004749; F:ribose-phosphate diphosphokinase activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0009116; P:nucleoside metabolism; IEA.  
 DR GO; GO:0003165; P:nucleotide biosynthesis; IEA.  
 DR InterPro; IPR000836; PRTtransferase.  
 DR InterPro; IPR005946; RibP\_Ppkin.  
 DR Pfam; PF00156; Pribosyltran; 1.  
 DR TIGRFAMs; TIGR01251; ribp\_ppkin; 1.  
 KW Transferase.  
 SQ SEQUENCE 386 AA; 41855 MW; 9FF565E4E3F8DD75 CRC64;  
 Query Match 68.4%; Score 39; DB 2; Length 386;  
 Best Local Similarity 70.0%; Pred. No. 72;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CVGSNKGAI 10  
 Db 264 CVGEVKGRI 273  
 RESULT 21  
 ID Q7QIK1 ANOGA PRELIMINARY; PRT; 393 AA.  
 AC Q7QIK1;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ENSANGP00000014395 (Fragment).  
 GN ORFNames=ENSANGG00000011906;  
 OS Anopheles gambiae str. PEST.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
 OC Anophelinae; Anopheles.  
 OX NCBI\_TaxID=180454;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PEST;  
 RG The Anopheles gambiae Sequence Committee;  
 RT "Anopheles gambiae re-annotation.";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PEST;  
 RG The Anopheles gambiae Sequence Committee;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAB01008980; EAA14479.2; -, Genomic DNA.

DR GO: 0005634; C:nucleus; IEA.  
 DR GO: 0004871; F:signal transducer activity; IEA.  
 DR GO: 0003700; F:transcription factor activity; IEA.  
 DR GO: 0006355; F:regulation of transcription, DNA-dependent; IEA.  
 DR GO: 0007165; F:signal transduction; IEA.  
 DR InterPro: IPR001067; Nuc translocat.  
 DR InterPro: IPR001610; PAC-  
 DR InterPro: IPR000014; PAS.  
 DR PRINTS: PRO0785; NCTRNSLOCATR.  
 DR SMART: SM00086; PAC; 1.  
 DR SMART: SM00091; PAS; 1.  
 DR PROSITE: PS01112; PAS; 1.  
 FT NON TER 393 393  
 SQ SEQUENCE 393 AA; 43995 MW; D6D026C9CBAA9D0 CRC64;  
 Query Match 68.4%; Score 39; DB 2; Length 393;  
 Best Local Similarity 60.0%; Pred. No. 74;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CVGSKNGAIC 10  
 Db 94 CMGSRGFGIC 103  
 RESULT 22  
 Q3V8N4 DROME PRELIMINARY; PRT; 513 AA.  
 AC Q3V8N4; Q95SKG;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE CG15097-PA, isoform A (GH18278p).  
 GN ORFNames=CG15097;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jastoli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195 (2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
 melanogaster euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskaas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the Drosophila melanogaster euchromatin:  
 a genomics perspective.";  
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 systematic review.";  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Berkeley Drosophila Genome Project;  
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskaas R., Smith E.,  
 RA Yu C., Rubin G.;  
 RT "Drosophila melanogaster release 4 sequence.";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RG FlyBase;  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN-Berkeley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003798; AAF57630.2; -; Genomic DNA.  
 DR EMBL; AY060733; AAL28281.1; -; mRNA.  
 DR Ensemble; CG15097; Drosophila melanogaster.  
 DR FlyBase; FBgn0034396; CG15097.  
 DR GO; GO:0005856; C:cytoskeleton; IEA.  
 DR GO; GO:0005535; F:protein binding; IEA.  
 DR InterPro; IPR011705; BACK.  
 DR InterPro; IPR00210; BTB\_POZ.  
 DR InterPro; IPR006651; Kelch.  
 DR InterPro; IPR006652; Kelch\_rep.  
 DR Pfam; PF07707; BACK; 1.  
 DR Pfam; PF00653; BTB; 1.

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DR Pfam: PF01344; Kelch_1; 6.
DR PRINTS; PR00501; KELCHREPEAT.
DR SMART; SM00612; Kelch; 6.
DR PROSITE; PS00097; BTB; 1.
SQ SEQUENCE 513 AA; 57551 MW; 20B9D4F732514834 CRC64;

Query Match      68.4%; Score 39; DB 2; Length 513;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1  CVGSKNGKAI 10
Db      |:|:|:|:|
         410 CIGENDSTWC 419

RESULT 23
O93296 CHICK PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -; mRNA.
DR HSSP; Q16019; IIYT.
DR SMR; O93296; 224-333.
DR Ensembl; ENSGALG0000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0003488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1_1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match      68.4%; Score 39; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  VGSNGKAI 9
Db      |||||
         459 VGSNGKAI 466

RESULT 24
Q9PVL1 CHICK PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

Query Match      68.4%; Score 39; DB 2; Length 569;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  VGSNGKAI 9
Db      |||||
         495 VGSNGKAI 502

RESULT 25
O86BF1 DROME PRELIMINARY; PRT; 617 AA.
AC O86BF1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG15097-PB isoform B.
GN Name=CG15097; ORFNames=CG15097;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]_TaxID=7227;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klanios I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W.N., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila  
melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review.";  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RG Berkeley Drosophila Genome Project;  
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,  
RA Hoskins R., Stapleton J., Pacleb J., Park S., Svirskas R., Smith E.,  
RA Yu C., Rubin G.;  
RT "Drosophila melanogaster release 4 sequence.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RG FlyBase;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003798; AAO41354.1; -; Genomic\_DNA.  
DR HSP; Q05516; 1CS3.  
DR Ensembl; CG15097; Drosophila melanogaster.  
DR FlyBase; FBgn0034396; CG15097.  
DR GO; GO:0005856; C:cytoskeleton; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR InterPro; IPR011705; BACK.

DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR006651; Kelch.  
DR InterPro; IPR006652; Kelch\_rep.  
DR Pfam; PF07707; BACK; 1.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch; 1.  
DR PRINTS; PR00501; KELCHREPEAT.  
DR SMART; SM00225; BTB; 1.  
DR SMART; SM00612; Kelch; 6.  
DR PROSITE; PS50097; BTB; 1.  
SQ SEQUENCE 617 AA; 68742 MW; 6005927B1B9DAE2C CRC64;  
  
Query Match 68.4%; Score 39; DB 2; Length 617;  
Best Local Similarity 50.0%; Pred. NO. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 CVGSKNGAIC 10  
|:|:|:|:|:  
DB 514 CIGGNDGTMC 523  
|:|:|:|:|:  
  
RESULT 26  
QBIH99 DROME PRELIMINARY; PRT; 620 AA.  
AC QBIH99;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE AT24465p (Fragment).  
GN ORFNames=CG15097;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
RA Celniker S.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BT001347; AAN71102.1; -; mRNA.  
DR HSP; Q05516; 1CS3.  
DR FlyBase; FBgn0034396; CG15097.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR InterPro; IPR011705; BACK\_POZ.  
DR InterPro; IPR000210; BTB\_POZ.  
DR InterPro; IPR006651; Kelch.  
DR Pfam; PF07707; BACK; 1.  
DR Pfam; PF00651; BTB; 1.  
DR Pfam; PF01344; Kelch; 1; 6.  
DR PRINTS; PR00501; KELCHREPEAT.  
DR SMART; SM00225; BTB; 1.  
DR SMART; SM00612; Kelch; 6.  
DR PROSITE; PS50097; BTB; 1.  
FT NON TER 1  
SQ SEQUENCE 620 AA; 69068 MW; 47CAD3F3B3A57871 CRC64;  
  
Query Match 68.4%; Score 39; DB 2; Length 620;  
Best Local Similarity 50.0%; Pred. NO. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 CVGSKNGAIC 10  
|:|:|:|:|:  
DB 517 CIGGNDGTMC 526  
|:|:|:|:|:  
  
RESULT 27  
Q98SGO\_XENLA

Q98SGO\_XENLA PRELIMINARY; PRT; 693 AA.  
Q98SGO;  
AC Q98477; 28-123, 383-492.  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Beta-amyloid precursor protein A.  
GN Name-app;  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP MEDLINE SEQUENCE.  
RX MEDLINE-21610087; PubMed11744158; DOI=10.1016/S0169-328X(01)00279-0;  
RA Van den Hurk W.H.; Bloemen M.; Martens G.J.M.;  
RT "Expression of the gene encoding the beta-amyloid precursor protein  
RT APP in Xenopus laevis.";  
RL Brain Res. Mol. Brain Res. 97:13-20(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Van den Hurk W.H.;  
RL Thesis (2001), Department of Biological Sciences, University of  
RL Nijmegen, Nijmegen, Netherlands.  
RL EMBL; AJ298150; CAC37193.1; -; mRNA.  
DR HSSP; Q16019; 1H23.  
DR SMR; Q98SGO; 27-122, 383-492.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR008154; A4\_extra.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR PRINTS; PR00204; BETAAMYLOID.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
KW Signal.  
FT SIGNAL. 1 19 Potential.  
SQ SEQUENCE 693 AA; 78567 MW; CAF1DF655C1AB653 CRC64;  
  
Query Match 68.4%; Score 39; DB 2; Length 693;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 VGSNKGAI 9  
DB 618 VGSNKGAI 625  
|||||  
RESULT 28  
QSR477\_PONPY  
ID QSR477\_PONPY PRELIMINARY; PRT; 695 AA.  
AC QSR477;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein DKF2p459D212.  
GN Name=DKF2p459D212;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Cortex;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

EMBL; CR861380; CAH93439.1; -; mRNA.  
DR SMR; QSR477; 28-123, 124-189, 385-494.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR008154; A4\_extra.  
DR InterPro; IPR001255; Beta-APP.  
DR InterPro; IPR012282; Cytochrome c\_r.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYLOID.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 695 AA; 78626 MW; 0BF5DD9BA2213E49 CRC64;  
  
Query Match 68.4%; Score 39; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 VGSNKGAI 9  
DB 620 VGSNKGAI 627  
|||||  
RESULT 29  
Q6RH29\_CANFA  
ID Q6RH29\_CANFA PRELIMINARY; PRT; 695 AA.  
AC Q6RH29;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Beta amyloid protein isoform APP695.  
GN Name=beta APP;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Nakata M.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY498707; AAR97727.1; -; mRNA.  
DR HSSP; Q16019; 1BA4.  
DR SMR; Q6RH29; 28-123, 124-189, 385-494.  
DR Ensembl; ENSCAFG0000008557; Canis familiaris.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005488; F:binding; IEA.  
DR InterPro; IPR008155; A4\_APP.  
DR InterPro; IPR008154; A4\_extra.  
DR InterPro; IPR001255; Beta-APP.  
DR Pfam; PF02177; A4\_EXTRA; 1.  
DR Pfam; PF03494; Beta-APP; 1.  
DR PRINTS; PR00203; AMYLOIDA4.  
DR PRINTS; PR00204; BETAAMYLOID.  
DR SMART; SM00006; A4\_EXTRA; 1.  
DR PROSITE; PS00319; A4\_EXTRA; 1.  
DR PROSITE; PS00320; A4\_INTRA; 1.  
SQ SEQUENCE 695 AA; 78649 MW; 718CA42A9F9E6C10 CRC64;  
  
Query Match 68.4%; Score 39; DB 2; Length 695;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 VGSNKGAI 9  
DB 620 VGSNKGAI 627  
|||||

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RESULT 30
Q56JK3 CANFA
ID Q56JK3_CANFA PRELIMINARY; PRT; 695 AA.
AC Q56JK3;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Beta-amyloid protein 695.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;
RT "Relationship between canine dementia and Alzheimer's disease.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY926582; AAX81911.1; -; mRNA.
SQ SEQUENCE 695 AA; 78748 MW; 5A253E0DB677875A CRC64;

Query Match 68.4%; Score 39; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 620 VGSNKGAI 627
|||||

RESULT 31
Q5GR78 MOUSE
ID Q5GR78_MOUSE PRELIMINARY; PRT; 695 AA.
AC Q5GR78;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Amyloid beta (A4) protein.
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC070409; AAH70409.1; -; mRNA.
SQ SEQUENCE 695 AA; 78442 MW; 0DE93FA56FB20F3A CRC64;

Query Match 68.4%; Score 39; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 620 VGSNKGAI 627
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RESULT 32
Q9DGJ8 CHICK
ID Q9DGJ8_CHICK PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-amyloid protein 695 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sarasa M., Rodolosse A., Sorribas V.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289218; AAG00593.1; -; mRNA.
DR HSP; Q16019, 11YT.
DR SMR; Q9DGJ8; 28-123, 124-189, 385-494.
DR Ensembl; ENSGALG0000015770; Gallus gallus.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 620 VGSNKGAI 627
|||||

RESULT 33
Q98SF9 XENLA
ID Q98SF9_XENLA PRELIMINARY; PRT; 695 AA.
AC Q98SF9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-amyloid precursor protein B.
GN Name=app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```



RX MEDLINE=21610087; PubMed=11744158; DOI=10.1016/S0169-328X(01)00279-0;  
 RA Van den Hurk W.H., Bloemen M., Martens G.J.M.;  
 RT "Expression of the gene encoding the beta-amyloid precursor protein  
 RT APP in *Xenopus laevis*.";  
 RL Brain Res. Mol. Brain Res. 97:13-20(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Van den Hurk W.H.;  
 RL Thesis (2001), Department of Biological Sciences, University of  
 RL Nijmegen, Nijmegen, Netherlands.  
 DR EMBL; AJ298151; CAC37194.1; -; mRNA.  
 DR HSSP; Q16019; 1H23.  
 DR SMR; Q98SF9; 27-122, 385-494.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAMYLOID.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 KW SIGNAL.  
 FT SIGNAL 1 19 Potential.  
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;  
  
 Query Match 68.4%; Score 39; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 VGSNKGAI 9  
 DB 620 VGSNKGAI 627  
  
 RESULT 34  
 Q7ZXQ0 XENLA  
 ID Q7ZXQ0\_XENLA PRELIMINARY; PRT; 695 AA.  
 AC Q7ZXQ0;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE MGCS2816 protein.  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OC NCBI\_TaxID=8355;  
 RN [1]\_TaxID=8355;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC044324; AAH44324.1; -; mRNA.  
 DR HSSP; Q16019; 1H23.  
 DR SMR; Q7ZXQ0; 27-122, 385-494.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4\_EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAMYLOID.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR PROSITE; PS00319; A4\_EXTRA; 1.  
 DR PROSITE; PS00320; A4\_INTRA; 1.  
 SQ SEQUENCE 695 AA; 78803 MW; C1BD8AACCC3356B05 CRC64;  
  
 Query Match 68.4%; Score 39; DB 2; Length 695;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 VGSNKGAI 9  
 DB 620 VGSNKGAI 627  
  
 RESULT 35  
 Q57394 NARJA  
 ID Q57394\_NARJA PRELIMINARY; PRT; 699 AA.  
 AC Q57394;  
 DT 01-JUN-1998 (TRENBLrel. 06, Created)  
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE EL amyloid protein 699.  
 GN Name=el app699; (Electric ray).  
 OS Närke japonica (Electric ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squala; Hypnosquala; Pristiogaster; Batoidea;  
 OC Torpediniformes; Narcinoidei; Narkidae; Närke.  
 OC NCBI\_TaxID=62965;  
 RN [1]\_TaxID=62965;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Electric lobe;  
 RX MEDLINE=98129705; PubMed=9461486;  
 RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,  
 RA Suzuki T.;  
 RT "cDNA isolation of Alzheimer's amyloid precursor protein from  
 RT cholinergic nerve terminals of the electric organ of the electric  
 RT ray.";  
 RL Biochem. J. 330:29-33(1998).  
 RL EMBL; AB005544; BAA24230.1; -; mRNA.  
 DR HSSP; Q16019; 1H23.  
 DR SMR; Q57394; 40-135, 136-201, 389-498.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR008155; A4\_APP.  
 DR InterPro; IPR008154; A4\_extra.

DR InterPro; IPR001255; Beta-APP.  
 DR Pfam; PF02177; A4 EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR SMART; SM00006; A4 EXTRA; 1.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4 INTRA; 1.  
 SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 68.4%; Score 39; DB 2; Length 699;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 |||||  
 DB 624 VGSNKGAI 631

RESULT 36  
 Q56JK4 CANPA  
 ID Q56JK4 CANPA PRELIMINARY; PRT; 714 AA.  
 AC Q56JK4;  
 DT 10-MAY-2005 (TReMBLrel. 30, Created)  
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
 DE Beta-amyloid protein 714.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Gallego C., Sanchez-Diaz R., Sarasa L., Sarasa M.;  
 RT "Relationship between canine dementia and Alzheimer's disease."  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AY926581; AAX81910.1; -; mRNA.  
 SQ SEQUENCE 714 AA; 80826 MW; 50DDE51FB9E90EC5 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 714;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 |||||  
 DB 639 VGSNKGAI 646

RESULT 37  
 Q6P6Q5 RAT  
 ID Q6P6Q5 RAT PRELIMINARY; PRT; 733 AA.  
 AC Q6P6Q5;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE App protein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Prostate;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 DR EMBL; BC062082; AAH62082.1; -; mRNA.  
 DR HSSP; Q16019; 1AAP.  
 DR SMR; Q6P6Q5; 28-123, 124-189, 287-342, 441-550.  
 DR Ensembl; ENSRNOG000006997; Rattus norvegicus.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR InterPro; IPR008155; A4 APP.  
 DR InterPro; IPR008154; A4 extra.  
 DR InterPro; IPR001255; Beta-APP.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR Pfam; PF02177; A4 EXTRA; 1.  
 DR Pfam; PF03494; Beta-APP; 1.  
 DR Pfam; PF00014; Kunitz\_BPTI; 1.  
 DR PRINTS; PR00203; AMYLOIDA4.  
 DR PRINTS; PR00759; BASICPTASE.  
 DR PRINTS; PR00204; BETAAMYLOID.  
 DR PRODOM; PD000222; Prot\_inh\_Kunz-m; 1.  
 DR SMART; SM00006; A4\_EXTRA; 1.  
 DR SMART; SM00131; KU; 1.  
 DR PROSITE; PS00319; A4 EXTRA; 1.  
 DR PROSITE; PS00320; A4 INTRA; 1.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS00279; BPTI\_KUNITZ\_2; 1.  
 SQ SEQUENCE 733 AA; 82797 MW; 8538F36FF73762F1 CRC64;

Query Match 68.4%; Score 39; DB 2; Length 733;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 |||||  
 DB 658 VGSNKGAI 665

RESULT 38  
 A4\_FUGRU  
 ID A4\_FUGRU STANDARD; PRT; 737 AA.  
 AC Q93279;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:  
 DE Beta-amyloid protein (Beta-APP) (A-beta)].  
 GN Name=APP;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=9825138; PubMed=9599080; DOI=10.1016/S0378-1119(98)00032-8;

RA Villard L., Tassone F., Crnogorac-Jurcovic T., Clancy K., Gardiner K.;  
 RT "Analysis of pufferfish homologues of the AT-rich human APP gene.";  
 CC Gene 210:17-24(1998).  
 CC -!- FUNCTION: Functional neuronal receptor which couples to  
 CC intracellular signaling pathway through the GTP-binding protein  
 CC G(O) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the APP family.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; AF090120; AAD13392.1; -; Genomic\_DNA.  
 CC DR HSP; P10646; IIRH.  
 CC DR SMR; O93279; 29-124, 440-542.  
 CC DR Ensembl; SINFUG00000150276; Fugu rubripes.  
 CC DR InterPro; IPR008155; A4\_APP.  
 CC DR InterPro; IPR008154; A4\_extra.  
 CC DR InterPro; IPR001255; Beta-APP.  
 CC DR PANTHER; PTHR10083:SF6; Beta-APP; 5.  
 CC DR Pfam; PF02177; A4\_EXTRA; 1.  
 CC DR Pfam; PF03494; Beta-APP; 1.  
 CC DR Pfam; PF00014; Kunitz BPTI; 1.  
 CC DR PRINTS; PR00203; AMYLOIDA4.  
 CC DR PRINTS; PR00759; BASICPTASE.  
 CC DR PRINTS; PR00204; BETAAMYLOID.  
 CC DR ProDom; PD000222; Prot\_Inh\_Kunz-m; 1.  
 CC DR SMART; SM00006; A4\_EXTRA; 1.  
 CC DR SMART; SM00131; KU; 1.  
 CC DR PROSITE; PS00319; A4\_EXTRA; 1.  
 CC DR PROSITE; PS00320; A4\_INTRA; 1.  
 CC DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 CC DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
 CC KW Amyloid; Glycoprotein; Protease inhibitor; Serine protease inhibitor;  
 FT Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 737 Alzheimer's disease amyloid A4 protein  
 FT homolog.  
 FT CHAIN 639 681 Beta-amyloid protein (Potential).  
 FT TOPO\_DOM 19 668 Extracellular (Potential).  
 FT TRANSMEM 669 689 Potential.  
 FT TOPO\_DOM 690 737 Cytoplasmic (Potential).  
 FT DOMAIN 286 344 BPTI/Kunitz inhibitor.  
 FT SITE 300 301 Reactive bond.  
 FT SITE 726 729 Clathrin-binding (By similarity).  
 FT CARBOHYD 522 522 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 290 340 By similarity.  
 FT DISULFID 299 323 By similarity.  
 FT DISULFID 315 336 By similarity.  
 FT SEQUENCE 737 AA; 82857 MW; 6FAD01E2E3B2B7E2 CRC64;  
 SQ  
 Query Match 68.4%; Score 39; DB 1; Length 737;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNGKAI 9  
 Db 662 VGSNGKAI 669  
 RESULT 39  
 Q91963 9PIPI  
 ID Q91963 9PIPI PRELIMINARY; PRT; 747 AA.  
 AC Q91963.  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE APP747.

GN Name=APP747;  
 OS Xenopus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodidae.  
 OC NCBI\_TaxID=8353;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93129227; PubMed=1282805;  
 RA Okado H., Okamoto H.;  
 RT "A Xenopus homologue of the human beta-amyloid precursor protein:  
 RT biochemical regulation of its gene expression.";  
 RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC EMBL; S52417; AAB24853.1; -; mRNA.  
 CC DR HSP; Q16019; LH23.  
 CC DR SMR; Q91963; 26-119, 283-338, 437-546.  
 CC DR GO; GO:0016021; C:integral to membrane; IEA.  
 CC DR GO; GO:0005488; F:binding; IEA.  
 CC DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 CC DR InterPro; IPR008155; A4\_APP.  
 CC DR InterPro; IPR008154; A4\_extra.  
 CC DR InterPro; IPR001255; Beta-APP.  
 CC DR InterPro; IPR002223; Prot\_Inh\_Kunz-m.  
 CC DR Pfam; PF02177; A4\_EXTRA; 1.  
 CC DR Pfam; PF03494; Beta-APP; 1.  
 CC DR Pfam; PF00014; Kunitz BPTI; 1.  
 CC DR PRINTS; PR00203; AMYLOIDA4.  
 CC DR PRINTS; PR00759; BASICPTASE.  
 CC DR PRINTS; PR00204; BETAAMYLOID.  
 CC DR ProDom; PD000222; Prot\_Inh\_Kunz-m; 1.  
 CC DR SMART; SM00131; KU; 1.  
 CC DR PROSITE; PS00319; A4\_EXTRA; 1.  
 CC DR PROSITE; PS00320; A4\_INTRA; 1.  
 CC DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 CC DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 1.  
 CC SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;  
 Query Match 68.4%; Score 39; DB 2; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNGKAI 9  
 Db 672 VGSNGKAI 679  
 RESULT 40  
 Q56JK2 STECO  
 ID Q56JK2 STECO PRELIMINARY; PRT; 749 AA.  
 AC Q56JK2.  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Beta-amyloid protein 749.  
 OS Stenella coeruleoalba (Striped dolphin).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;  
 OC Odontoceti; Delphinidae; Stenella.  
 CC NCBI\_TaxID=9737;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Gallego C., Sarasa M.;  
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.  
 CC EMBL; AY926583; AAX81912.1; -; mRNA.  
 CC DR GO; GO:0016021; C:integral to membrane; IEA.  
 CC DR GO; GO:0005488; F:binding; IEA.  
 CC DR GO; GO:0020037; F:heme binding; IEA.  
 CC DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 CC DR GO; GO:0006118; P:electron transport; IEA.  
 CC SQ SEQUENCE 749 AA; 84542 MW; 426599887C2A95D6 CRC64;  
 DE APP747.

Query Match 68.4%; Score 39; DB 2; Length 749;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 |||||  
 Db 674 VGSNKGAI 681

Search completed: January 28, 2006, 00:58:52  
 Job time : 81 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 28, 2006, 00:52:36 ; Search time 78 Seconds  
(without alignments)  
56.331 Million cell updates/sec

Title: US-09-018-194A-4  
Perfect score: 57  
Sequence: 1 CVGSNKGATC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	2	Aaw45346 Peptide u
2	57	100.0	10	2	Aay39233 Cyclic pe
3	57	100.0	10	4	Aag64004 Human bet
4	57	100.0	10	5	Abb07973 Beta-amyl
5	57	100.0	10	9	Adv44279 Cyclic p7
6	39	68.4	8	2	Aaw45343 Beta-amyl
7	39	68.4	8	2	Aay39236 Beta-amyl
8	39	68.4	8	4	Aag64001 Human bet
9	39	68.4	8	5	Abb07970 Human bet
10	39	68.4	8	9	Adv44276 Human bet
11	39	68.4	9	8	ADI35977 Human bet
12	39	68.4	9	8	ADI36001 Amyloid b
13	39	68.4	9	8	ADI35858 Amyloid b
14	39	68.4	9	8	ADI35988 Amyloid b
15	39	68.4	10	4	AAB46234 Human APP
16	39	68.4	10	4	AAB46235 Human APP
17	39	68.4	10	4	AAB46236 Human APP
18	39	68.4	11	5	Aau93989 Human bet
19	39	68.4	11	7	ADe10850 Chimeric
20	39	68.4	11	7	Adm39755 B-cell pe
21	39	68.4	11	8	ADG63950 Recombina
22	39	68.4	11	8	ADP73484 Alzheimer
23	39	68.4	11	8	Adri2777 Human bet
24	39	68.4	12	9	ADz08893 Human bet

98 39 68.4 38 8 ADJ71493 N-termina  
99 39 68.4 38 8 ADJ71485 N-termina  
100 39 68.4 38 8 ADU24436 Novel glu

ALIGNMENTS

RESULT 1  
AAW45346  
ID AAW45346 standard; peptide; 10 AA.  
XX AC  
XX AC AAW45346;  
XX AC  
DT 08-MAY-1998 (first entry)  
XX  
XX Peptide used for diagnosing and treating Alzheimer's disease.  
XX  
XX Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;  
KW neurotrophin receptor p75; p75NTR; nerve growth factor; NGF.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Disulfide-bond 1..10  
FT /note= "disulphide bond"  
FT  
XX  
XX WO9737228-A1.  
XX  
XX PD  
XX PD 09-OCT-1997.  
XX  
XX PF 28-MAR-1997; 97WO-US004966.  
XX  
XX PR 29-MAR-1996; 96US-00625765.  
XX  
XX PA (UYBO-) UNIV BOSTON.  
XX  
XX PI Gilchrest BA, Yaar M;  
XX  
XX WPI; 1997-512306/47.  
XX  
XX Evaluating risk of individual to develop Alzheimer's - uses cultured  
PT epidermal melanocyte(s), also useful for developing therapies for neuro-  
PT degenerative diseases.  
XX  
XX Claim 14; Page 21; 42pp; English.  
XX  
XX The invention relates to methods of therapy for Alzheimer's disease using  
CC peptides (AAW45343-6) that bind to the neurotrophin receptor p75 nerve  
CC growth factor receptor (NGFR) and competitively inhibit the binding of a  
CC beta-amyloid to the p75 NGFR. Also described is a new method for  
CC evaluating the risk of an individual to develop Alzheimer's disease  
CC cultured neural crest-derived melanocytes. The methods can be used for  
CC diagnosing and treating Alzheimer's disease and other neurodegenerative  
CC diseases mediated by beta-amyloid protein, or by aberrant activation of  
CC the low affinity NGFR localised on neural cell surfaces, such as  
CC autoimmune encephalomyelitis, Huntington's disease, cortico-basal  
CC degeneration, progressive supra-nuclear palsy, Gerotman-Shaussler  
CC Scheinker syndrome, Neimann-Pick disease, and progressive supranuclear  
CC palsy. In the diagnostic tests, the human melanocytes, which are easily  
CC obtainable from skin biopsies, are good model cells for the study and  
CC diagnosis of Alzheimer's disease  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CVGSNKGGAIC 10  
Db 1 CVGSNKGGAIC 10  
|||||

RESULT 2  
AAV39233  
ID AAV39233 standard; peptide; 10 AA.  
XX AC  
XX AAV39233;  
XX  
DT 23-NOV-1999 (first entry)  
XX  
XX Cyclic peptide used to inhibit p75-NTR mediated apoptosis.  
DE  
XX  
XX Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor;  
KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;  
KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;  
KW skin colour; alopecia areata; male pattern baldness.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "N-terminus is attached via a peptide bond to the  
FT C-terminus amino acid at position 10"  
FT Modified-site 10  
FT /note= "C-terminus is attached via a peptide bond to the  
FT N-terminus amino acid at position 1"  
XX  
XX WO9939728-A2.  
XX  
XX PD 12-AUG-1999.  
XX  
XX PF 03-FEB-1999; 99WO-US002362.  
XX  
XX PR 04-FEB-1998; 98US-00018194.  
XX  
XX PA (UYBO-) UNIV BOSTON.  
XX  
XX PI Gilchrest BA, Yaar M, Eller M;  
XX  
XX WPI; 1999-539950/45.  
XX  
XX Controlling or manipulating melanocyte and keratinocyte cell death,  
PT useful for treating, e.g. alopecia areata.  
XX  
XX Claim 4; Page 39; 67pp; English.  
XX  
XX This sequence is a cyclic peptide which competes with and competitively  
CC inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR).  
CC p75NTR is a low affinity nerve growth factor (NGF) receptor which is  
CC expressed by melanocytes and keratinocytes of the basal epidermis.  
CC Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2  
CC protein. If the receptor is occupied by appropriate ligands e.g.  
CC neurotrophins, apoptosis is inhibited. Other examples of appropriate  
CC ligands include this cyclic peptide. This peptide is based on the  
CC sequence of the binding fragment of beta-amyloid, which binds to p75NTR  
CC in Alzheimer's disease. This cyclic peptide can be used in methods to  
CC control or manipulate keratinocyte or melanocyte cell death. The methods  
CC involve using this peptide or peptides AAV39234-Y39235 to bind as a  
CC pseudo-ligand to the p75 neurotrophin receptor, inhibiting apoptosis. The  
CC new method can induce or maintain hair growth, hair colour or skin  
CC colour. Inducing or maintaining hair growth is useful for treating  
CC alopecia areata or male pattern baldness in vertebrates  
XX  
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0042;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CVGSNKGGAIC 10  
Db 1 CVGSNKGGAIC 10  
|||||

RESULT 3  
 AAG64004  
 ID AAG64004 standard; peptide; 10 AA.  
 XX  
 AC AAG64004;  
 XX  
 DT 31-AUG-2001 (first entry)  
 XX  
 DE Human beta-amyloid-derived cyclic peptide #2.  
 XX  
 DE Human; beta-amyloid; nootropic; neuroprotective; anticonvulsant;  
 KW p75 nerve growth factor receptor; inhibitor; Alzheimer's disease;  
 KW neurodegenerative disease; cyclic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..10  
 FT /note= "the peptide has a cyclic structure as a result of  
 FT the bonding between the two cysteine residues"  
 XX  
 XX US6242416-B1.  
 PN 05-JUN-2001.  
 PD  
 PD 29-SEP-1998; 98US-00163095.  
 PF 29-MAR-1996; 96US-00625765.  
 XX 28-MAR-1997; 97WO-US004966.  
 PR  
 PR (UYBO-) UNIV BOSTON.  
 PA Gilchrist BA, Yaar M;  
 XX WPI; 2001-380482/40.  
 DR  
 DR Inhibition of beta-amyloid binding to the p75 nerve growth factor  
 PT receptor using polypeptides, useful in the diagnosis and treatment of  
 PT e.g. Alzheimer's disease.  
 XX  
 PS Claim 2; Col 18; 16pp; English.  
 XX  
 CC The invention relates to methods for inhibiting binding of beta-amyloid  
 CC to the p75 nerve growth factor receptor. The methods comprise contacting  
 CC the cell with a substance that binds to the p75 nerve growth factor  
 CC receptor. The methods are useful in the diagnosis and treatment of  
 CC Alzheimer's disease and other neurodegenerative diseases mediated by beta  
 CC -amyloid protein, or by aberrant activation of the low affinity nerve  
 CC growth factor receptor localised on neural cell surfaces. Such diseases  
 CC include autoimmune encephalomyelitis, Huntington's disease, Pick's  
 CC disease, corticobasal degeneration, progressive supranuclear palsy,  
 CC Gerotman-Shauleser Scheinker syndrome, Niemann-Pick disease and Down's  
 CC syndrome. The present sequence is a cyclic peptide comprising a fragment  
 CC of the human beta-amyloid protein to which a cysteine residue has been  
 CC added at each end. The peptide inhibits binding of beta-amyloid to the  
 CC p75 nerve growth factor receptor  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 0.0042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVGSNKGATC 10  
 DB |||||||||  
 1 CVGSNKGATC 10  
 RESULT 4  
 ABB07973  
 ID ABB07973 standard; peptide; 10 AA.

XX ABB07973;  
 AC 12-AUG-2002 (first entry)  
 DT  
 DE Beta-amyloid p75NTR binding inhibiting cyclic peptide.  
 XX  
 DE Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic;  
 KW Alzheimer's disease; neurotrophin receptor; NTR; human; cyclic.  
 KW  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1..10  
 FT /note= "disulphide bridge"  
 FT  
 XX US2002051988-A1.  
 PN 02-MAY-2002.  
 PD  
 PD 29-MAY-2001; 2001US-00866898.  
 PF 29-MAR-1996; 96US-00625765.  
 XX 28-MAR-1997; 97WO-US004966.  
 PR 29-SEP-1998; 98US-00163095.  
 PR  
 PR (UYBO-) UNIV BOSTON.  
 PA Gilchrist BA, Yaar M;  
 XX WPI; 2002-443695/47.  
 DR  
 DR Evaluating risk of an individual to develop Alzheimer's disease using  
 PT cultured neural crest-derived melanocytes and methods of therapy for  
 PT Alzheimer's disease using peptides that bind to the neurotrophin  
 PT receptor.  
 XX  
 PS Claim 4; Page 8; 19pp; English.  
 XX  
 CC The invention relates to a method of inhibiting beta-amyloid binding to  
 CC the p75 nerve growth factor receptor (NGFR) of a cell. The method  
 CC involves contacting the cell with a substance having the amino acid  
 CC sequence lysine-glycine-lysine or lysine-glycine-alanine. The substance  
 CC binds to the p75 NGFR resulting in the inhibition of beta-amyloid protein  
 CC or beta-amyloid peptide binding to the p75 NGFR. The invention is useful  
 CC for evaluating the risk of an individual to develop Alzheimer's disease  
 CC and methods of therapy for Alzheimer's disease using peptides that bind  
 CC to the neurotrophin receptor (NTR) and competitively inhibit the binding  
 CC of beta-amyloid to the receptor. In vitro methods are also provided for  
 CC screening substances and identifying those capable of inhibiting, or  
 CC decreasing cell apoptosis mediated by beta-amyloid. The present sequence  
 CC represents a cyclic peptide that competes for p75NTR binding with the  
 CC beta-amyloid peptide  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 57; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 0.0042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVGSNKGATC 10  
 DB |||||||||  
 1 CVGSNKGATC 10  
 RESULT 5  
 ADV44279  
 ID ADV44279 standard; peptide; 10 AA.  
 XX  
 AC ADV44279;  
 XX  
 DT 10-MAR-2005 (first entry)  
 DT  
 XX

DE Cyclic p75NTR-binding peptide of the invention SEQ ID NO:4.  
 XX beta-amyloid; melanocyte; nootropic; neuroprotective; Alzheimers disease;  
 KW degeneration; neurological disease; cyclic; neurotrophin receptor;  
 KW p75NTR.  
 OS Synthetic.  
 XX US2004254110-A1.  
 PN 16-DEC-2004.  
 XX 24-FEB-2004; 2004US-00785924.  
 XX 29-MAR-1996; 96US-00625765.  
 PR 28-MAR-1997; 97WO-0004966.  
 PR 29-SEP-1998; 98US-00163095.  
 PR 29-MAY-2001; 2001US-00866898.  
 XX (UYBO-) UNIV BOSTON.  
 PA Gilchrest BA, Yaar M;  
 XX WPI; 2005-064094/07.  
 DR New peptide inhibiting beta-amyloid binding to neural-crest-derived cells  
 XX or beta-amyloid mediated apoptosis of neural-crest-derived cells, useful  
 PT for diagnosing and treating Alzheimer's disease.  
 PT Claim 43; SEQ ID NO 4; 16pp; English.  
 XX The invention relates to a novel peptide that inhibits beta-amyloid  
 CC binding to neural crest-derived cells or beta-amyloid mediated apoptosis  
 CC of neural crest-derived cells, comprising amino acid sequence lysine-  
 CC glycine-lysine or lysine-glycine-alanine. The peptide is a cyclic  
 CC peptide. A peptide of the invention has nootropic and neuroprotective  
 CC activity. The methods and compositions of the present invention are  
 CC useful for evaluating risk to, diagnosing and treating Alzheimer's  
 CC disease using neural crest-derived melanocytes and peptides that bind the  
 CC neurotrophin receptor (p75NTR) and inhibit binding of beta-amyloid to the  
 CC p75NTR. The present sequence represents a cyclic peptide of the  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 100.0%; Score 57; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0042;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CVGSNKGATC 10  
 DB |||||||||  
 1 CVGSNKGATC 10  
 RESULT 6  
 AA45343  
 ID AA45343 standard; peptide; 8 AA.  
 XX AA45343;  
 AC 08-MAY-1998 (first entry)  
 XX Beta-amyloid fragment (residues 24-31).  
 DE Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;  
 KW neurotrophin receptor p75; p75NTR; cyclic.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9737228-A1.  
 PN 09-OCT-1997.  
 XX

XX 28-MAR-1997; 97WO-US004966.  
 XX 29-MAR-1996; 96US-00625765.  
 PR (UYBO-) UNIV BOSTON.  
 PA Gilchrest BA, Yaar M;  
 XX WPI; 1997-512306/47.  
 DR Evaluating risk of individual to develop Alzheimer's - uses cultured  
 XX epidermal melanocyte(s), also useful for developing therapies for neuro-  
 PT degenerative diseases.  
 PT Disclosure; Page 10; 42pp; English.  
 XX The present sequence represents residues 24 to 31 of beta-amyloid. A  
 CC cyclic peptide was synthesised by attaching two cysteine residues to the  
 CC beginning and the end of the fragment. The invention relates to a new  
 CC method for evaluating the risk of an individual to develop Alzheimer's  
 CC disease using cultured neural crest-derived melanocytes. Also described  
 CC are methods of therapy for Alzheimer's disease using peptides (AAW45343-  
 CC 6) that bind to the neurotrophin receptor p75 nerve growth factor  
 CC receptor (NGFR) and competitively inhibit the binding of a beta-amyloid  
 CC to the p75 NGFR. The methods can be used for diagnosing and treating  
 CC Alzheimer's disease and other neurodegenerative diseases mediated by beta  
 CC -amyloid protein, or by aberrant activation of the low affinity NGFR  
 CC localised on neural cell surfaces, such as autoimmune encephalomyelitis,  
 CC Huntington's disease, cortico-basal degeneration, progressive supra-  
 CC nuclear palsy, Gerotman-Straussler Scheinker syndrome, Neimann-Pick  
 CC disease, and progressive supranuclear palsy. In the diagnostic tests, the  
 CC human melanocytes, which are easily obtainable from skin biopsies, are  
 CC good model cells for the study and diagnosis of Alzheimer's disease  
 XX Sequence 8 AA;  
 SQ Query Match 68.4%; Score 39; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 DB |||||||  
 1 VGSNKGAI 8  
 RESULT 7  
 AAY39236  
 ID AAY39236 standard; peptide; 8 AA.  
 XX AAY39236;  
 AC 23-NOV-1999 (first entry)  
 XX Beta-amyloid fragment for generation of p75NTR inhibiting peptides.  
 DE p75NTR; p75 neurotrophin receptor; nerve growth factor; NGF; melanocyte;  
 KW keratinocyte; apoptosis; Bcl-2; beta-amyloid fragment;  
 KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;  
 XX skin colour; alopecia areata; male pattern baldness.  
 XX Synthetic.  
 OS WO9939728-A2.  
 XX 12-AUG-1999.  
 PD 03-FEB-1999; 99WO-US002362.  
 XX 04-FEB-1998; 98US-00018194.  
 XX (UYBO-) UNIV BOSTON.  
 XX



PI Gilchrest BA, Yaar M, Eller M;  
 XX WPI; 1999-539950/45.  
 XX Controlling or manipulating melanocyte and keratinocyte cell death,  
 PT useful for treating, e.g. alopecia areata.  
 XX  
 PS Disclosure; Page 15; 67pp; English.  
 XX  
 CC This sequence is amino acids 24-31 of beta-amyloid. This sequence can be  
 CC used to generate cyclic peptide AAV39233. The cyclic peptide competes  
 CC with and competitively inhibits beta-amyloid binding to the p75  
 CC neurotrophin receptor (p75NTR). p75NTR is a low affinity nerve growth  
 CC factor (NGF) receptor which is expressed by melanocytes and keratinocytes  
 CC of the basal epidermis. Apoptosis can be inhibited by p75NTR via the  
 CC upregulation of the Bcl-2 protein. If the receptor is occupied by  
 CC appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other  
 CC examples of appropriate ligands include this cyclic peptide. This peptide  
 CC is based on the sequence of the binding fragment of beta-amyloid, which  
 CC binds to p75NTR in Alzheimer's disease. This cyclic peptide can be used  
 CC in methods to control or manipulate keratinocyte or melanocyte cell  
 CC death. The methods involve using this peptide or peptides AAV39234-Y39235  
 CC to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting  
 CC apoptosis. The new method can induce or maintain hair growth, hair colour  
 CC or skin colour. Inducing or maintaining hair growth is useful for  
 CC treating alopecia areata or male pattern baldness in vertebrates  
 XX  
 SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
 Db 1 VGSNKGAI 8  
 |||||

RESULT 8  
 AAG64001  
 ID AAG64001 standard; peptide; 8 AA.  
 XX  
 AC AAG64001;  
 DT 31-AUG-2001 (first entry)  
 XX  
 DE Human beta-amyloid peptide.  
 XX  
 KW Human; beta-amyloid; nootropic; neuroprotective; anticonvulsant;  
 KW p75 nerve growth factor receptor; inhibitor; Alzheimer's disease;  
 KW neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6242416-B1.  
 XX  
 PD 05-JUN-2001.  
 XX  
 PF 29-SEP-1998; 98US-00163095.  
 XX  
 PR 29-MAR-1996; 96US-00625765.  
 PR 28-MAR-1997; 97WO-US004966.  
 XX  
 PA (UYBO-) UNIV BOSTON.

XX Gilchrest BA, Yaar M;  
 XX WPI; 2001-380482/40.  
 XX  
 XX Inhibition of beta-amyloid binding to the p75 nerve growth factor  
 PT receptor using polypeptides, useful in the diagnosis and treatment of  
 PT e.g. Alzheimer's disease.  
 XX

PS Claim 2; Col 7; 16pp; English.  
 XX  
 CC The invention relates to methods for inhibiting binding of beta-amyloid  
 CC to the p75 nerve growth factor receptor. The methods comprise contacting  
 CC the cell with a substance that binds to the p75 nerve growth factor  
 CC receptor. The methods are useful in the diagnosis and treatment of  
 CC Alzheimer's disease and other neurodegenerative diseases mediated by beta  
 CC -amyloid protein, or by aberrant activation of the low affinity nerve  
 CC growth factor receptor localised on neural cell surfaces. Such diseases  
 CC include autoimmune encephalomyelitis, Huntington's disease, Pick's  
 CC disease, corticobasal degeneration, progressive supranuclear palsy,  
 CC Gerotman-Straussler Scheinker syndrome, Niemann-Pick disease and Down's  
 CC syndrome. The present sequence is a fragment of the human beta-amyloid  
 CC protein. It may be used to produce a cyclic decapeptide that inhibits  
 CC binding of beta-amyloid to the p75 nerve growth factor receptor  
 XX  
 SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9  
 Db 1 VGSNKGAI 8  
 |||||

RESULT 9  
 ABB07970  
 ID ABB07970 standard; peptide; 8 AA.  
 XX  
 AC ABB07970;  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Beta-amyloid peptide fragment (residues 24-31).  
 XX  
 KW Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic;  
 KW Alzheimer's disease; neurotrophin receptor; human.  
 XX  
 OS Homo sapiens.

XX US2002051988-A1.  
 XX 02-MAY-2002.  
 XX  
 PF 29-MAY-2001; 2001US-00866898.  
 XX  
 PR 29-MAR-1996; 96US-00625765.  
 PR 28-MAR-1997; 97WO-US004966.  
 PR 29-SEP-1998; 98US-00163095.  
 XX  
 PA (UYBO-) UNIV BOSTON.  
 XX  
 PI Gilchrest BA, Yaar M;  
 XX  
 DR WPI; 2002-443695/47.

XX  
 PT Evaluating risk of an individual to develop Alzheimer's disease using  
 PT cultured neural crest-derived melanocytes and methods of therapy for  
 PT Alzheimer's disease using peptides that bind to the neurotrophin  
 PT receptor.  
 XX

PS Claim 4; Page 4; 19pp; English.

XX The invention relates to a method of inhibiting beta-amyloid binding to  
 CC the p75 nerve growth factor receptor (NGFR) of a cell. The method  
 CC involves contacting the cell with a substance having the amino acid  
 CC sequence lysine-glycine-lysine or lysine-glycine-alanine. The substance  
 CC binds to the p75 NGFR resulting in the inhibition of beta-amyloid protein  
 CC or beta-amyloid peptide binding to the p75 NGFR. The invention is useful  
 CC for evaluating the risk of an individual to develop Alzheimer's disease  
 CC and methods of therapy for Alzheimer's disease using peptides that bind

CC to the neurotrophin receptor and competitively inhibit the binding of  
 CC beta-amyloid to the receptor. In vitro methods are also provided for  
 CC screening substances and identifying those capable of inhibiting, or  
 CC decreasing cell apoptosis mediated by beta-amyloid. The present sequence  
 CC represents a beta-amyloid peptide fragment  
 XX  
 SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 DB 1 VGSNKGAI 8  
 |||||

## RESULT 10

ADV44276  
 ID ADV44276 standard; peptide; 8 AA.

XX  
 AC ADV44276;

XX  
 DT 10-MAR-2005 (first entry)

XX  
 DE Human beta-amyloid fragment SEQ ID NO:1.

XX beta-amyloid; melanocyte; nootropic; neuroprotective; Alzheimers disease;  
 KW degeneration; neurological disease.

XX Homo sapiens.

XX US2004254110-A1.

XX 16-DEC-2004.

XX 24-FEB-2004; 2004US-00785924.

XX 29-MAR-1996; 96US-00635765.

XX 28-MAR-1997; 97WO-US004965.

XX 29-SEP-1998; 98US-00163095.

XX 29-MAY-2001; 2001US-00866898.

XX (UYBO-) UNIV BOSTON.

XX Gilchrist BA, Yaar M;

XX WPI; 2005-064094/07.

XX  
 PT New peptide inhibiting beta-amyloid binding to neural-crest-derived cells  
 PT or beta-amyloid mediated apoptosis of neural-crest-derived cells, useful  
 PT for diagnosing and treating Alzheimer's disease.

XX Claim 43; SEQ ID NO 1; 16pp; English.

XX The invention relates to a novel peptide that inhibits beta-amyloid  
 CC binding to neural crest-derived cells or beta-amyloid mediated apoptosis  
 CC of neural crest-derived cells, comprising amino acid sequence lysine-  
 CC glycine-lysine or lysine-glycine-alanine. The peptide is a cyclic  
 CC peptide. A peptide of the invention has nootropic and neuroprotective  
 CC activity. The methods and compositions of the present invention are  
 CC useful for evaluating risk to, diagnosing and treating Alzheimer's  
 CC disease using neural crest-derived melanocytes and peptides that bind the  
 CC neurotrophin receptor (p75NTR) and inhibit binding of beta-amyloid to the  
 CC p75NTR. The present sequence represents a peptide fragment of beta-  
 CC amyloid, used to produce a cyclic decapeptide of the invention.

XX Sequence 8 AA;

Query Match 68.4%; Score 39; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 DB 1 VGSNKGAI 8  
 |||||

## RESULT 11

ADI35977  
 ID ADI35977 standard; peptide; 9 AA.

XX  
 AC ADI35977;

XX 22-APR-2004 (first entry)

XX Amyloid beta peptide SEQ ID NO:131.

XX amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 KW Alzheimer's disease.

XX Synthetic.

XX WO2004006861-A2.

XX 22-JAN-2004.

XX 16-JUL-2003; 2003WO-US022280.

XX 17-JUL-2002; 2002US-0396245P.

XX (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX Chain DG, Fitzer-Attas C;

XX WPI; 2004-122759/12.

XX New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 PT or treating Alzheimer's disease.

XX Example 6; SEQ ID NO 131; 69pp; English.

XX The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acid obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.

XX Sequence 9 AA;

Query Match 68.4%; Score 39; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 DB 1 VGSNKGAI 8  
 |||||

## RESULT 12

ADI36001  
ID ADI36001 standard; peptide; 9 AA.

XX AC ADI36001;

XX DT 22-APR-2004 (first entry)

XX DE Amyloid beta peptide SEQ ID NO:155.

XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
XX KW Alzheimer's disease.

XX OS Synthetic.

XX PN WO2004006861-A2.

XX PD 22-JAN-2004.

XX PF 16-JUL-2003; 2003WO-US022280.

XX PR 17-JUL-2002; 2002US-0396245P.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX PI Chain DG, Fitzer-Attas C;

XX DR WPI; 2004-122759/12.

XX PT New amyloid beta peptide, useful for preparing a composition for  
PT preventing the formation or progression of amyloid plaques for preventing  
PT or treating Alzheimer's disease.

XX PS Example 6; SEQ ID NO 155; 69pp; English.

XX CC The present invention describes an isolated amyloid beta peptide or its  
CC homologue which is selected by a method comprising: (a) determining the  
CC binding value of each amino acid of a subsequence of amyloid beta peptide  
CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
CC determining the resulting score of all amino acids of the subsequence,  
CC based on the binding value of each amino acid obtained in step (1); and  
CC (c) comparing the resulting score to a preselected value. Also described:  
CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
CC for immunisation of an individual based on the HLA haplotype of the  
CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
CC peptide to an individual based on the HLA haplotype of the individual;  
CC and (6) preventing the formation or progression of amyloid plaques. The  
CC amyloid beta peptide has neuroprotective activity, and can be used in  
CC vaccines. The amyloid beta peptide is useful for preparing a composition  
CC for preventing the formation or progression of amyloid plaques for  
CC preventing or treating Alzheimer's disease. The present sequence  
CC represents an amyloid beta (Abeta) peptide, which is used in an example  
CC from the present invention.

XX SQ Sequence 9 AA;

Query Match 68.4%; Score 39; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

DB 2 VGSNKGAI 9

## RESULT 13

ADI35858  
ID ADI35858 standard; peptide; 9 AA.

XX AC ADI35858;

XX

DT 22-APR-2004 (first entry)

XX DE Amyloid beta peptide SEQ ID NO:12.

XX KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
XX KW Alzheimer's disease.

XX OS Synthetic.

XX PN WO2004006861-A2.

XX PD 22-JAN-2004.

XX PF 16-JUL-2003; 2003WO-US022280.

XX PR 17-JUL-2002; 2002US-0396245P.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.

XX PI Chain DG, Fitzer-Attas C;

XX DR WPI; 2004-122759/12.

XX PT New amyloid beta peptide, useful for preparing a composition for  
PT preventing the formation or progression of amyloid plaques for preventing  
PT or treating Alzheimer's disease.

XX PS Example 1; SEQ ID NO 12; 69pp; English.

XX CC The present invention describes an isolated amyloid beta peptide or its  
CC homologue which is selected by a method comprising: (a) determining the  
CC binding value of each amino acid of a subsequence of amyloid beta peptide  
CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
CC determining the resulting score of all amino acids of the subsequence,  
CC based on the binding value of each amino acid obtained in step (1); and  
CC (c) comparing the resulting score to a preselected value. Also described:  
CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
CC for immunisation of an individual based on the HLA haplotype of the  
CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
CC peptide to an individual based on the HLA haplotype of the individual;  
CC and (6) preventing the formation or progression of amyloid plaques. The  
CC amyloid beta peptide has neuroprotective activity, and can be used in  
CC vaccines. The amyloid beta peptide is useful for preparing a composition  
CC for preventing the formation or progression of amyloid plaques for  
CC preventing or treating Alzheimer's disease. The present sequence  
CC represents an amyloid beta (Abeta) peptide, which is used in an example  
CC from the present invention.

XX SQ Sequence 9 AA;

Query Match 68.4%; Score 39; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

DB 1 VGSNKGAI 8

## RESULT 14

ADI35988  
ID ADI35988 standard; peptide; 9 AA.

XX AC ADI35988;

XX DT 22-APR-2004 (first entry)

XX DE Amyloid beta peptide SEQ ID NO:142.

XX

KW amyloid beta peptide; vaccine; immunisation; neuroprotective;  
 KW Alzheimer's disease.  
 XX Synthetic.  
 OS  
 XX WO2004006861-A2.  
 XX  
 XX PD 22-JAN-2004.  
 XX  
 XX PF 16-JUL-2003; 2003WO-US022280.  
 XX  
 XX PR 17-JUL-2002; 2002US-0396245P.  
 XX  
 XX PA (MIND-) MINDSET BIOPHARMACEUTICALS INC.  
 XX  
 XX PI Chain DG, Fitzer-Attas C;  
 XX  
 XX DR WPI; 2004-122759/12.  
 XX  
 XX PT New amyloid beta peptide, useful for preparing a composition for  
 PT preventing the formation or progression of amyloid plaques for preventing  
 PT or treating Alzheimer's disease.  
 XX  
 XX PS Example 6; SEQ ID NO 142; 69pp; English.  
 XX  
 CC The present invention describes an isolated amyloid beta peptide or its  
 CC homologue which is selected by a method comprising: (a) determining the  
 CC binding value of each amino acid of a subsequence of amyloid beta peptide  
 CC upon binding to a HLA class I and/or class II molecule of interest; (b)  
 CC determining the resulting score of all amino acids of the subsequence,  
 CC based on the binding value of each amino acids obtained in step (1); and  
 CC (c) comparing the resulting score to a preselected value. Also described:  
 CC (1) a vaccine comprising the isolated amyloid beta peptide and a carrier  
 CC or diluent; (2) determining T-cell epitopes within amyloid beta peptide;  
 CC (3) predicting the reaction of an individual to a vaccine; (4) matching a  
 CC vaccine comprising a beta amyloid or homologue peptide to an individual,  
 CC for immunisation of an individual based on the HLA haplotype of the  
 CC individual; (5) a kit for matching a vaccine comprising amyloid beta  
 CC peptide to an individual based on the HLA haplotype of the individual;  
 CC and (6) preventing the formation or progression of amyloid plaques. The  
 CC amyloid beta peptide has neuroprotective activity, and can be used in  
 CC vaccines. The amyloid beta peptide is useful for preparing a composition  
 CC for preventing the formation or progression of amyloid plaques for  
 CC preventing or treating Alzheimer's disease. The present sequence  
 CC represents an amyloid beta (Abeta) peptide, which is used in an example  
 CC from the present invention.  
 XX  
 XX SQ Sequence 9 AA;  
 Query Match 68.4%; Score 39; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0;  
 QY 2 VGSNKGAI 9  
 Db 1 VGSNKGAI 8  
 |||||  
 |||||  
 RESULT 15  
 AAB46234  
 ID AAB46234 standard; peptide; 10 AA.  
 XX  
 XX AC AAB46234;  
 XX  
 XX DT 04-APR-2001 (first entry)  
 XX  
 XX DE Human APP derived immunogenic peptide #30.  
 XX  
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX  
 XX OS Homo sapiens.

XX WO200072880-A2.  
 XX  
 XX PD 07-DEC-2000.  
 XX  
 XX PF 26-MAY-2000; 2000WO-US014810.  
 XX  
 XX PR 28-MAY-1999; 99US-00322289.  
 XX  
 XX PA (NEUR-) NEURALAB LTD.  
 XX  
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX  
 XX DR WPI; 2001-032104/04.  
 XX  
 XX PT Preventing or treating a disease associated with amyloid deposits,  
 XX especially Alzheimer's disease, comprises administering amyloid specific  
 XX antibody.  
 XX  
 XX PS Disclosure; Fig 19; 143pp; English.  
 XX  
 CC This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 XX SQ Sequence 10 AA;  
 Query Match 68.4%; Score 39; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;  
 Matches 8; Conservative 0;  
 QY 2 VGSNKGAI 9  
 Db 3 VGSNKGAI 10  
 |||||  
 |||||  
 RESULT 16  
 AAB46235  
 ID AAB46235 standard; peptide; 10 AA.  
 XX  
 XX AC AAB46235;  
 XX  
 XX DT 04-APR-2001 (first entry)  
 XX  
 XX DE Human APP derived immunogenic peptide #31.  
 XX  
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PD WO200072880-A2.  
 XX  
 XX PR 07-DEC-2000.  
 XX  
 XX PF 26-MAY-2000; 2000WO-US014810.  
 XX  
 XX PR 28-MAY-1999; 99US-00322289.  
 XX  
 XX PA (NEUR-) NEURALAB LTD.  
 XX  
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.  
 XX Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.  
 XX  
 XX Disclosure; Fig 19; 143pp; English.  
 XX  
 XX This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises  
 CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 68.4%; Score 39; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5,7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 Db |||||  
 2 VGSNKGAI 9  
 RESULT 17  
 AAB46236  
 ID AAB46236 standard; peptide; 10 AA.  
 XX  
 XX AAB46236;  
 AC  
 XX  
 XX 04-APR-2001 (first entry)  
 DT Human APP derived immunogenic peptide #32.  
 XX  
 XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;  
 XX Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;  
 KW amyloid precursor protein; Alzheimer's disease.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200072880-A2.  
 PN  
 XX 07-DEC-2000.  
 PD  
 XX 26-MAY-2000; 2000WO-US014810.  
 PF  
 XX 28-MAY-1999; 99US-00322289.  
 PR  
 XX (NEUR-) NEURALAB LTD.  
 XX  
 XX Schenk DB, Bard F, Vasquez NJ, Yednock T;  
 XX WPI; 2001-032104/04.  
 DR  
 XX Preventing or treating a disease associated with amyloid deposits,  
 PT especially Alzheimer's disease, comprises administering amyloid specific  
 PT antibody.  
 XX  
 XX Disclosure; Fig 19; 143pp; English.  
 PS  
 XX This invention describes a novel method of preventing or treating a  
 CC disease associated with amyloid deposits of amyloid precursor protein  
 CC (APP) Abeta fragments in the brain of a patient, which comprises

CC administering to the patient: (a) an antibody that binds to Abeta, the  
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc  
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing  
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent  
 CC that induces an immunogenic response against residues 1-3 to 7-11 of  
 CC Abeta. The products of the invention have neurotropic and neuroprotective  
 CC activity. The method is also useful for monitoring a course of treatment  
 CC being administered to a patient e.g. active and passive immunization. The  
 CC methods are useful for prophylactic and therapeutic treatment of  
 CC Alzheimer's disease  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 68.4%; Score 39; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5,7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 Db |||||  
 1 VGSNKGAI 8  
 RESULT 18  
 AAU93989  
 ID AAU93989 standard; peptide; 11 AA.  
 XX  
 XX AAU93989;  
 AC  
 XX  
 XX 02-JUL-2002 (first entry)  
 DT Human beta-amyloid B cell epitope #3.  
 XX  
 XX Immunogenic; hepatitis B cell epitope; T cell epitope; immunostimulant.  
 KW  
 KW vaccine; B cell epitope; T cell epitope; immunostimulant.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200214478-A2.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 16-AUG-2001; 2001WO-US041759.  
 PF  
 XX 16-AUG-2000; 2000US-0225843P.  
 PR  
 XX 22-AUG-2000; 2000US-0228667P.  
 PR  
 XX 15-AUG-2001; 2001US-00930915.  
 XX  
 XX (APOV-) APOVIA INC.  
 XX  
 XX Birkett AJ;  
 PI  
 XX WPI; 2002-257601/30.  
 DR  
 XX Novel recombinant hepatitis B core (HBC) protein (I), displaying one or  
 PT more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or  
 PT C-terminus, or having a heterologous linker for a conjugated epitope in  
 PT (L), and containing a Cys residue at, or near, the C-terminus that  
 XX confers enhanced stability to the particles. A vaccine comprising (I) is  
 XX useful for inducing an immune response in an inoculated host animal, by  
 XX inoculating a host animal with the vaccine, and maintaining that  
 XX inoculated animal for a time period sufficient for that animal to develop  
 XX an immune response. The immunogenic particles formed using (I) are  
 XX substantially free of binding to nucleic acids, and are most stable than  
 XX the particle formed from otherwise identical HBC chimera that lacks the C-  
 XX terminal residue or in which a C-terminal Cys is replaced by another  
 XX residue. The chimera particles are most stable on storage in aqueous

CC compositions that are particles of similar sequence that lack any C-  
 CC terminal Cys residues. The chimera molecule exhibits the self-assembly not  
 CC exhibiting the nucleic acid binding of those native particles, and  
 CC excellent B cell and T cell immunogenicities. The chimera particles are  
 CC typically prepared in higher yield than similar particles that are free  
 CC of a C-terminal Cys. The particles are often far more immunogenic than  
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of  
 CC particles assembled from the chimera molecules are enhanced as compared to  
 CC similar particles assembled from chimera molecules lacking at least one C-  
 CC terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles amino  
 CC acid sequences and related sequences of the invention  
 XX  
 XX  
 SQ Sequence 11 AA;

Query Match 68.4%; Score 39; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 DB 3 VGSNKGAI 10  
 |||||

RESULT 19  
 ADE10850  
 ID ADE10850 standard; peptide; 11 AA.

XX  
 AC ADE10850;

XX  
 DT 29-JAN-2004 (first entry)

XX  
 DE Chimeric hepatitis B virus related B-cell epitope seqid 84.

XX  
 KW hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;  
 KW recombinant hepatitis B core chimeric protein; HBC chimeric protein;  
 KW hepatitis B infection; T-cell stimulator; B-cell epitope.

XX  
 OS Unidentified.

XX  
 FN US2003198645-A1.

XX  
 PD 23-OCT-2003.

XX  
 PF 21-FEB-2003; 2003US-00372076.

XX  
 PR 21-FEB-2002; 2002US-00080299.

XX  
 PR 21-FEB-2002; 2002US-00082014.

XX  
 PA (PAGE/) PAGE M.  
 PA (FRIE/) FRIEDE M.

XX  
 PI Page M, Friede M;

XX  
 DR WPI; 2003-852775/79.

XX  
 PT Treating chronic hepatitis B infection by administering a T cell-  
 PT stimulating vaccine containing immunogenic particles having recombinant  
 PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein  
 PT molecules.

XX  
 PS Disclosure; SEQ ID NO 84; 111pp; English.

XX  
 CC The invention describes a method of treating chronic hepatitis comprising  
 CC administering to a patient a T cell-stimulating amount of a vaccine  
 CC comprising immunogenic particles dissolved or dispersed in a diluent,  
 CC where the immunogenic particles consists of recombinant hepatitis B core  
 CC (HBC) chimeric protein molecules, and maintaining the patient to induce T  
 CC cells activated against HBC. The methods and compositions of the present  
 CC invention are useful for treating chronic hepatitis B infection. This is  
 CC the amino acid sequence of a chimeric hepatitis B virus related B-cell  
 CC epitope useful for expression within the HBV chimera at the N-terminus,  
 CC within the immunogenic loop and/or at the C-terminus.

SQ Sequence 11 AA;

Query Match 68.4%; Score 39; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
 DB 3 VGSNKGAI 10  
 |||||

RESULT 20

ADM39755

ID ADM39755 standard; peptide; 11 AA.

XX  
 AC ADM39755;

XX  
 DT 03-JUN-2004 (first entry)

XX  
 DE B-cell peptide epitope expressed by HBC chimera Seq 87.

XX  
 KW immunogenic; avian hepatitis B virus; nucleocapsid;  
 KW self assembled particle; immunogen; inoculum; vaccine; immunostimulant;  
 KW antibacterial; virucidal; B-cell epitope.

XX  
 OS Unidentified.

XX  
 FN WO2003072722-A2.

XX  
 PD 04-SEP-2003.

XX  
 PF 21-FEB-2003; 2003WO-US005315.

XX  
 PR 21-FEB-2002; 2002US-0359129P.

XX  
 PA (APOV-) APOVIA INC.

XX  
 PI Birkett AJ, Peck B;

XX  
 DR WPI; 2003-679948/64.

XX  
 PT New recombinant chimera avian hepatitis B core protein molecule, useful as  
 PT an immunogen for inducing a B cell or T cell response to produce  
 PT antibodies, or as a vaccine against pathogens.

XX  
 PS Disclosure; SEQ ID NO 87; 278pp; English.

XX  
 CC This invention relates to novel recombinant immunogenic chimeric avian  
 CC hepatitis B core (AHBC) nucleocapsid proteins. Specifically, it refers to  
 CC an AHBC protein that has been engineered to display an immunogenic B cell  
 CC or T cell epitope, exhibit enhanced stability and an absence of nucleic  
 CC acid binding as a self assembled particle. The present invention  
 CC describes the chimeric AHBC protein as truncated at the C-terminus and  
 CC containing introduced cysteine residues that confers an enhanced  
 CC stability in aqueous solution, an increased yield and more immunogenicity  
 CC than similar conjugates that lack N- or C-terminal cysteines.

XX  
 CC Furthermore, a reduction in the number of positively charged residues  
 CC (lysine and arginine) towards the C-terminus prepares self-assembled  
 CC particles that are substantially free of nucleic acid binding. As such,  
 CC these chimeric particles can be used as immunogens of an inoculum that  
 CC induce a B cell or T cell response in an animal to produce antibodies. It  
 CC can also be useful for developing a vaccine to protect against the  
 CC pathogen from which the heterologous epitope or the haptens is derived.  
 CC Accordingly, these compositions exhibit immunostimulant, antibacterial  
 CC and virucidal activities. This peptide sequence is an exemplary B-cell  
 CC epitope peptide immunogen useful for both linkage to the linker residue  
 CC after expression of a contemplated chimera and for expression within an  
 CC HBC chimera of the invention.

SQ Sequence 11 AA;

Query Match 68.4%; Score 39; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
Db 3 VGSNKGAI 10

## RESULT 21

ADG63950  
ID ADG63950 standard; peptide; 11 AA.

XX AC ADG63950;

XX DT 11-MAR-2004 (first entry)

XX XX Recombinant chimera hepatitis B core protein immunogenic epitope #75.

XX KW Recombinant chimera hepatitis B core protein; HBC; immunogenic epitope;  
XX KW HBC immunodominant loop; immune response.

XX OS Unidentified.

XX PN US2003185858-A1.

XX PD 02-OCT-2003.

XX PF 21-FEB-2002; 2002US-00082014.

XX PR 15-AUG-2001; 2001US-00930915.

XX XX (BIRK/) BIRKETT A J.

XX PI Birkett AJ;

XX WPI; 2004-031988/03.

XX PT Recombinant chimera hepatitis B core protein molecule useful for preparing  
PT vaccine or inoculum includes peptide-bonded heterologous immunogenic  
PT epitope at N-terminus in the hepatitis B core immunodominant loop or C-  
PT terminus of the chimera.

XX PS Disclosure; SEQ ID NO 83; 110pp; English.

XX CC The invention relates to a recombinant chimera hepatitis B core (HBC)  
CC protein molecule that includes a peptide-bonded heterologous immunogenic  
CC epitope at the N-terminus in the HBC immunodominant loop or the C-  
CC terminus of the chimera, or a heterologous linker residue for a conjugated  
CC epitope present in the loop. The invention also relates to an immunogenic  
CC particle comprising the recombinant hepatitis B core chimera protein  
CC molecules, a vaccine comprising the immunogenic particles dissolved or  
CC dispersed in a diluent, a nucleic acid that encodes a recombinant HBC  
CC protein molecule or its variant, analogue, or complement and a method for  
CC inducing an immune response in an inoculated host animal comprising  
CC inoculating a host animal with a vaccine and maintaining the inoculated  
CC animal for a period of time sufficient to enable development of an immune  
CC response. The recombinant chimera hepatitis B core protein molecule is  
CC used in an immunogenic particle for preparing a vaccine useful for  
CC inducing an immune response in an inoculated host animal. This sequence  
CC represents an HBC protein immunogenic B cell epitope of the invention.

XX SQ Sequence 11 AA;

Query Match 68.4%; Score 39; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
Db 3 VGSNKGAI 10

## RESULT 22

ADP73484

ID ADP73484 standard; peptide; 11 AA.

XX AC ADP73484;

XX DT 09-SEP-2004 (first entry)

XX DE Alzheimer's disease B cell epitope of gene beta-amyloid, SEQ ID 97.  
XX KW transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;  
XX KW enhanced stability; hepatotropic; virucide; immunology;  
XX KW protein engineering; immunogen; vaccine; Hepatitis B infection.

XX OS Unidentified.

XX PN WO2004053091-A2.

XX PD 24-JUN-2004.

XX PF 10-DEC-2003; 2003WO-US039164.

XX PR 10-DEC-2002; 2002US-0432123P.

XX PA (APOV-) APOVIA INC.

XX PI Lyons K, Birkett AJ, Haron JA;

XX WPI; 2004-468859/44.

XX PT New recombinant chimera hepatitis B core (HBC) protein molecules useful in  
PT the fields of immunology and protein engineering, in particular as an  
PT immunogen in a vaccine for Hepatitis B infections.

XX PS Disclosure; SEQ ID NO 97; 338pp; English.

XX CC The invention relates to a novel recombinant chimeric Hepatitis B virus  
CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues  
CC in length. The chimeric protein is engineered for both enhanced stability  
CC of self-assembled particles and the substantial absence of nucleic acid  
CC binding by the particles. The invention further comprises: a recombinant  
CC HBC protein chimeric molecule that has a length of 135-365 amino acid  
CC residues and contains four peptide-linked amino acid residue sequence  
CC domains from the N-terminus that are denominated Domains I, II, III and  
CC IV. The invention also provides nucleic acids, polypeptides, host cells,  
CC chimeric compositions of the invention have hepatotropic and virucide  
CC activities. The methods and compositions of the present invention are  
CC useful in the fields of immunology and protein engineering, in particular  
CC for using a chimeric hepatitis B virus nucleocapsid protein as an  
CC immunogen in a vaccine for Hepatitis B infections. This sequence  
CC represents a Hepatitis B virus nucleocapsid (core) protein related  
CC polypeptide of the invention.

XX SQ Sequence 11 AA;

Query Match 68.4%; Score 39; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
|||||||  
Db 3 VGSNKGAI 10

## RESULT 23

ADRI2777

ID ADRI2777 standard; peptide; 11 AA.

XX AC ADRI2777;

XX DT 04-NOV-2004 (first entry)

XX DE Human beta-amyloid protein B cell epitope #3.

KW Human; chronic hepatitis; Hbc; nucleocapsid core protein; vaccine;  
 KW immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; CD4+ cell;  
 KW cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;  
 KW TLR-4; TLR-9; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004156863-A1.  
 XX  
 XX 12-AUG-2004.  
 PD  
 XX  
 XX 01-OCT-2003; 2003US-00677074.  
 XX  
 XX 21-FEB-2002; 2002US-00080299.  
 PR  
 PR 21-FEB-2002; 2002US-00082014.  
 PR  
 XX 21-FEB-2003; 2003US-00372076.  
 XX  
 PA (PAGE/) PAGE M.  
 PA (FRIE/) FRIEDE M.  
 PA (SCHM/) SCHMIDT A. E.  
 PA (STOB/) STOBBER D.  
 XX  
 XX Page M, Friede M, Schmidt AE, Stober D;  
 XX WPI; 2004-603322/58.  
 DR  
 XX  
 XX Treating chronic hepatitis, by administering vaccine comprising  
 PT immunogenic particles having recombinant hepatitis B core chimeric  
 PT protein molecules, that stimulates T cell, to patient chronically  
 PT infected with hepatitis B virus.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 84; 117pp; English.  
 XX  
 XX The invention relates to treating chronic hepatitis, by administering a  
 CC vaccine comprising immunogenic particles having recombinant hepatitis B  
 CC core (Hbc) chimeric protein molecules (where truncated Hbc molecules are  
 CC linked N-terminally or C-terminally to an immunogenic epitope), that  
 CC stimulate T cell production, to a patient chronically infected with  
 CC hepatitis B virus, and maintaining patient for time sufficient to induce  
 CC T cells activated against Hbc. The chimeric proteins are still capable  
 CC self-assembling into particles upon expression in a host cell and are  
 CC substantially free of binding to nucleic acids, and the particles display  
 CC enhanced stability. Also included is enhancing (M2) the production of one  
 CC or more of gamma-producing CD8+, CD4+ T cells and cytotoxic T lymphocytes  
 CC against hepatitis B virus, involving administering to a patient  
 CC chronically infected with hepatitis B virus, a T cell-stimulating amount  
 CC of a vaccine comprising immunogenic particles dissolved or dispersed in a  
 CC diluent containing one or both of an agonist of toll-like receptor 4 and  
 CC receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising Hbc  
 CC chimeric protein molecules and maintaining the patient for a sufficient  
 CC time to induce T cells activated against Hbc. The immunogenic epitopes  
 CC may be B cell or T cell epitopes. The chimeric vaccine is useful for  
 CC treating a patient chronically infected with hepatitis B virus. The  
 CC present sequence is a B cell epitope suitable for inclusion in the  
 CC chimeric protein of the invention.  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 68.4%; Score 39; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 Db |||||  
 3 VGSNKGAI 10  
 RESULT 24  
 ADZ08893  
 ID ADZ08893 standard; peptide; 12 AA.  
 XX  
 AC ADZ08893;  
 XX

DT 16-JUN-2005 (first entry)  
 XX Human beta-amyloid peptide (SEQ ID NO:118) probed with anti-amyloid IgG.  
 DE  
 XX amyloid; antibody engineering; antibody production;  
 KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;  
 KW autoimmune disease; Parkinsons disease;  
 KW acquired immune deficiency syndrome; multiple sclerosis; migraine;  
 KW dementia; infection; nontropic; neuroprotective; cytostatic;  
 KW antiallergic; Immunosuppressive; antiparkinsonian; antimigraine;  
 KW antimicrobial; anti-HIV; beta-amyloid.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2005028511-A2.  
 PN  
 XX 31-MAR-2005.  
 PD  
 XX 26-MAR-2004; 2004WO-US009522.  
 XX  
 XX 28-MAR-2003; 2003US-0458469P.  
 PR  
 PR 28-MAR-2003; 2003US-0458474P.  
 PR  
 PR 28-MAR-2003; 2003US-0458509P.  
 PR  
 PR 28-MAR-2003; 2003US-0458510P.  
 XX  
 PA (CENZ ) CENTOCOR INC.  
 PA (MERC/) MERCKEN M.  
 PA (BENS/) BENSON J M.  
 XX  
 XX Mercken M, Benson JM;  
 XX WPI; 2005-242565/25.  
 DR  
 XX New isolated mammalian anti-amyloid antibodies useful for treating  
 PT amyloid-associated disorders, such as Alzheimer's disease, cancer,  
 PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,  
 PT migraine and dementia.  
 XX  
 XX Example 4; SEQ ID NO 118; 306pp; English.  
 PS  
 CC The invention relates to at least one isolated mammalian amyloid antibody  
 CC comprising at least one variable region comprising at least one heavy  
 CC chain and at least one light chain, of a fully defined sequence of SEQ ID  
 CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:  
 CC (i) at least one isolated mammalian amyloid antibody that binds to the  
 CC same region of an amyloid polypeptide as an antibody comprising at least  
 CC one heavy chain or light chain complementarity determining region (CDR)  
 CC having the amino acid sequence of at least one of SEQ ID NO: 73-78 (ii)  
 CC at least one isolated mammalian amyloid antibody, comprising at least one  
 CC human CDR, where the antibody specifically binds at least one epitope  
 CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined  
 CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic  
 CC acid encoding at least one of any of the isolated mammalian amyloid  
 CC antibodies mentioned and having at least one human CDR of a fully defined  
 CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an  
 CC isolated nucleic acid vector comprising an isolated nucleic acid encoding  
 CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising  
 CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of  
 CC producing at least one amyloid antibody, (vii) a composition comprising  
 CC at least one of any of the isolated mammalian amyloid antibodies  
 CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an  
 CC anti-idiotypic antibody or fragment that specifically binds at least one  
 CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or  
 CC treating an amyloid related condition in a cell, tissue, organ or animal,  
 CC comprising contacting or administering a composition comprising at least  
 CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or  
 CC animal, (x) a medical device comprising at least one amyloid antibody  
 CC mentioned, where the device is suitable for contacting or administering  
 CC at least one amyloid antibody, (xi) an article of manufacture for human  
 CC pharmaceutical or diagnostic use, comprising packaging material and a  
 CC container comprising a solution or a lyophilized form of at least one of  
 CC the amyloid antibodies mentioned, and (xii) a method of producing at  
 CC least one of the isolated mammalian amyloid antibodies, comprising



CC providing a host cell or transgenic animal or transgenic plant or plant  
CC cell capable of expressing the antibody in recoverable amounts. The  
CC methods and compositions of the present invention are useful for  
CC producing therapeutic compositions and devices for treating amyloid-  
CC associated disorders, such as Alzheimer's disease, cancer, allergies,  
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,  
CC migraine, dementia and infections. This sequence represents a peptide  
CC from human beta-amyloid probed with anti-beta-amyloid IgG antibodies.  
XX  
SQ Sequence 12 AA;

Query Match 68.4%; Score 39; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 3 VGSNKGAI 10  
|||||

RESULT 25  
AAB91815  
ID AAB91815 standard; peptide; 14 AA.  
XX  
AC AAB91815;  
XX  
DT 22-JUN-2001 (first entry)  
XX  
DE Amyloid beta-protein fragment peptide SEQ ID NO:991.  
XX  
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200069900-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 17-MAY-2000; 2000WO-US013576.  
XX  
PR 17-MAY-1999; 99US-0134406P.  
PR 10-SEP-1999; 99US-0153406P.  
PR 15-OCT-1999; 99US-0159783P.  
XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX  
DR WPI; 2001-112059/12.  
XX  
PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX  
PS Disclosure; Page 519; 733pp; English.  
XX  
CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 14 AA;

Query Match 68.4%; Score 39; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
Db 3 VGSNKGAI 10  
|||||

RESULT 26  
AAB91782  
ID AAB91782 standard; peptide; 14 AA.  
XX  
AC AAB91782;  
XX  
DT 22-JUN-2001 (first entry)  
XX  
DE Amyloid beta-protein fragment peptide SEQ ID NO:958.  
XX  
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200069900-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 17-MAY-2000; 2000WO-US013576.  
XX  
PR 17-MAY-1999; 99US-0134406P.  
PR 10-SEP-1999; 99US-0153406P.  
PR 15-OCT-1999; 99US-0159783P.  
XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX  
DR WPI; 2001-112059/12.  
XX  
PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX  
PS Disclosure; Page 507; 733pp; English.  
XX  
CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 14 AA;

Query Match 68.4%; Score 39; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
| | | | |  
Db 3 VGSNKGAI 10

## RESULT 27

AAB91788  
ID AAB91788 standard; peptide; 14 AA.

XX

AC AAB91788;

XX 22-JUN-2001 (first entry)

XX

DE Amyloid beta-protein fragment peptide SEQ ID NO:964.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimide; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

PN 23-NOV-2000.

PD 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

PA Bridon DP, Erin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX

DR Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX Disclosure; Page 509; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention

XX Sequence 14 AA;

Query Match 68.4%; Score 39; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

| | | | |

Db 3 VGSNKGAI 10

## RESULT 28

ADG93166

ID ADG93166 standard; peptide; 14 AA.

XX

AC ADG93166;

XX

DT 11-MAR-2004 (first entry)

XX

DE Novel expression cassette-related polypeptide SeqID47.

XX expression cassette; high yield polypeptide production;

XX tandem polypeptide; inclusion body.

XX

OS Unidentified.

XX

PN WO2003100021-A2.

XX

PD 04-DEC-2003.

XX

PF 23-MAY-2003; 2003WO-US016643.

XX

PR 24-MAY-2002; 2002US-0383370P.

XX

PA (REST-) RESTORAGEN INC.

PA (HARL/) HARLEY S.

XX

PI Harley S, Williams JA, Luan P, Xia Y;

XX

DR WPI; 2004-035128/03.

XX

DR N-PSDB; ADG93186.

XX

PT New expression cassette comprising an operably linked nucleic acid

PT sequence, useful for producing a tandem polypeptide that forms an

PT inclusion body when expressed in a cell.

XX

PS Disclosure; SEQ ID NO 47; 157pp; English.

XX

CC This invention relates to a novel expression cassette and methods for  
CC high yield production of polypeptides. The cassette comprises an operably  
CC linked nucleic acid sequence, where the expression of the cassette  
CC produces a tandem polypeptide that forms an inclusion body when expressed  
CC in a cell. The expression cassette is useful for producing peptide and  
CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
CC inclusion body when expressed in a cell. The present sequence is that of  
CC a polypeptide which may be produced using the expression cassette of the  
CC invention.

XX Sequence 14 AA;

SQ

Query Match 68.4%; Score 39; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

| | | | |

Db 3 VGSNKGAI 10

## RESULT 29

ADJ65844

ID ADJ65844 standard; peptide; 14 AA.

XX

AC ADJ65844;

XX

DT 06-MAY-2004 (first entry)

XX

DE Amyloid Beta-peptide #2.

XX

KW expression cassette; tandem polypeptide; inclusion body;

XX inclusion body fusion partner; amyloid Beta-peptide.

OS Unidentified.  
 XX WO2003100022-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 23-MAY-2003; 2003WO-US016645.  
 XX  
 PR 24-MAY-2002; 2002US-0383212P.  
 XX  
 PA (REST-) RESTORAGEN INC.  
 XX  
 PI Xia Y, Peng L;  
 XX  
 XX WPI; 2004-035129/03.  
 DR N-PSDB; ADJ65864.  
 XX  
 PT New expression cassette comprising an operably linked nucleic acid  
 PT sequence, useful for producing a tandem polypeptide that forms an  
 PT inclusion body when expressed in a cell.  
 XX  
 PS Disclosure; SEQ ID NO 20; 132pp; English.  
 XX  
 CC The invention comprises an expression cassette which produces a tandem  
 CC polypeptide that form an inclusion body when expressed in a cell. The  
 CC expression cassette of the invention is useful for producing a peptide or  
 CC polypeptide in a cell, preferably a tandem polypeptide that forms an  
 CC inclusion body when expressed in a cell. The present amino acid sequence  
 CC represents a peptide which may be used in the construction of a tandem  
 CC polypeptide of the invention.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 68.4%; Score 39; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 Db 3 VGSNKGAI 10  
 |||||  
 RESULT 30  
 ABU63716  
 ID ABU63716 standard; peptide; 20 AA.  
 XX  
 AC ABU63716;  
 XX  
 DT 15-OCT-2003 (first entry)  
 XX  
 DE Rat amyloid beta 1-40 (Abeta1-40) peptide insulin cleavage product #9.  
 XX  
 KW Rat; amyloid beta; Abeta; amyloid fibril; amyloid plaque; neurotoxicity;  
 KW amyloid peptide-inactivating enzyme; hydrolysis; zinc metalloproteinase;  
 KW insulin degrading enzyme; IDE; insulysin; neprelysin; peptide therapy;  
 KW Alzheimer's disease; nootropic; neuroprotective.  
 XX  
 OS Rattus sp.  
 XX  
 PN US2003083277-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 26-FEB-2001; 2001US-00792079.  
 XX  
 PR 24-FEB-2000; 2000US-0184826P.  
 XX  
 PA (HERS/) HERSH L B.  
 XX  
 PI Hersh LB;  
 XX  
 XX WPI; 2003-576623/54.  
 DR  
 XX

PT Preventing formation or growth of amyloid fibrils or plaques without  
 PT causing neurotoxicity, useful for treating Alzheimer's disease, comprises  
 PT administering an amyloid peptide inactivating enzyme.  
 XX  
 PS Example 11; Page 9; 20pp; English.  
 XX  
 CC The invention discloses a method for preventing the formation or growth  
 CC of amyloid fibrils or plaques without causing neurotoxicity. The method  
 CC comprises administering an inactivation effective amount of an amyloid  
 CC peptide-inactivating enzyme to a mammal. The strategy is to hydrolyse the  
 CC amyloid beta (Abeta) peptides before they form amyloid plaques using the  
 CC zinc metalloproteinase insulin degrading enzyme (IDE), insulysin or  
 CC neprelysin. The methods and enzymes are useful for treating (e.g peptide  
 CC therapy) Alzheimer's disease. The enzymes are useful for inducing the  
 CC synthesis of endogenous amyloid inactivating enzymes, such as insulysin  
 CC or neprelysin, within the brain of the affected individuals. The sequence  
 CC presented is a Abeta1-40 peptide insulin cleavage product  
 XX  
 SQ Sequence 20 AA;  
 Query Match 68.4%; Score 39; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VGSNKGAI 9  
 Db 4 VGSNKGAI 11  
 |||||  
 RESULT 31  
 ADF55645  
 ID ADF55645 standard; peptide; 20 AA.  
 XX  
 AC ADF55645;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human A beta 1-40 insulysin cleavage fragment #9.  
 XX  
 KW amyloid plaque; neurotoxicity; amyloid peptide inactivating enzyme;  
 KW Alzheimer's disease; human; A beta 1-40; insulysin.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003165481-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 03-JUN-2002; 2002US-00159279.  
 XX  
 PR 24-FEB-2000; 2000US-0184826P.  
 PR 26-FEB-2001; 2001US-00792079.  
 XX  
 PA (HERS/) HERSH L B.  
 XX  
 PI Hersh LB;  
 XX  
 XX WPI; 2003-898030/82.  
 DR  
 XX  
 PT Preventing formation or growth of amyloid plaques without causing  
 PT neurotoxicity, useful for treating Alzheimer's disease, by generating a  
 PT vector comprising a DNA sequence encoding at least one amyloid peptide  
 PT inactivating enzyme.  
 XX  
 PS Example 11; SEQ ID NO 9; 36pp; English.  
 XX  
 CC The invention relates to a method of preventing formation or growth of  
 CC amyloid plaque without causing neurotoxicity which comprises generating a  
 CC recombinant viral or plasmid vector comprising a DNA sequence encoding at  
 CC least one amyloid peptide inactivating enzyme operably linked to a  
 CC promoter. The methods are useful for treating Alzheimer's disease by  
 CC increasing the activity of an amyloid inactivating enzyme. The present  
 CC sequence represents the amino acid sequence of a human A beta 1-40

```
CC insulysin cleavage fragment.
XX
SQ Sequence 20 AA;

Query Match      68.4%; Score 39; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 4 VGSNKGAI 11
|||||

RESULT 32
ABU63714
ID ABU63714 standard; peptide; 21 AA.
XX AC
XX ABU63714;
XX
XX 15-OCT-2003 (first entry)
XX
XX Rat amyloid beta 1-40 (Abeta1-40) peptide insulysin cleavage product #7.
XX
XX Rat; amyloid beta; Abeta; amyloid fibril; amyloid plaque; neurotoxicity;
XX amyloid peptide-inactivating enzyme; hydrolysis; zinc metalloproteinase;
XX insulin degrading enzyme; IDE; insulysin; neprilysin; peptide therapy;
XX Alzheimer's disease; neurotropic; neuroprotective.
XX
XX Rattus sp.
XX
XX US2003083277-A1.
XX
XX 01-MAY-2003.
XX
XX 26-FEB-2001; 2001US-00792079.
XX
XX 24-FEB-2000; 2000US-0184826P.
XX
XX (HERS/) HERSH L B.
XX
XX Hersh LB;
XX
XX WPI; 2003-576623/54.
XX
XX Preventing formation or growth of amyloid fibrils or plaques without
XX causing neurotoxicity, useful for treating Alzheimer's disease, comprises
XX administering an amyloid peptide inactivating enzyme.
XX
XX Example 11; Page 9; 20pp; English.
XX
XX The invention discloses a method for preventing the formation or growth
XX of amyloid fibrils or plaques without causing neurotoxicity. The method
XX comprises administering an inactivation effective amount of an amyloid
XX peptide-inactivating enzyme to a mammal. The strategy is to hydrolyse the
XX amyloid beta (Abeta) peptides before they form amyloid plaques using the
XX zinc metalloproteinase insulin degrading enzyme (IDE), insulysin or
XX neprilysin. The methods and enzymes are useful for treating (e.g peptide
XX therapy) Alzheimer's disease. The enzymes are useful for inducing the
XX synthesis of endogenous amyloid inactivating enzymes, such as insulysin
XX or neprilysin, within the brain of the affected individuals. The sequence
XX presented is a Abeta1-40 peptide insulysin cleavage product
XX
SQ Sequence 21 AA;

Query Match      68.4%; Score 39; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 5 VGSNKGAI 12
|||||

RESULT 33
ADF55643
ID ADF55643 standard; peptide; 21 AA.
XX AC
XX ADF55643;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human A beta 1-40 insulysin cleavage fragment #7.
XX
XX amyloid plaque; neurotoxicity; amyloid peptide inactivating enzyme;
XX Alzheimer's disease; human; A beta 1-40; insulysin.
XX
XX Homo sapiens.
XX
XX US2003165481-A1.
XX
XX 04-SEP-2003.
XX
XX 03-JUN-2002; 2002US-00159279.
XX
XX 24-FEB-2000; 2000US-0184826P.
XX
XX 26-FEB-2001; 2001US-00792079.
XX
XX (HERS/) HERSH L B.
XX
XX Hersh LB;
XX
XX WPI; 2003-898030/82.
XX
XX Preventing formation or growth of amyloid plaques without causing
XX neurotoxicity, useful for treating Alzheimer's disease, by generating a
XX vector comprising a DNA sequence encoding at least one amyloid peptide
XX inactivating enzyme.
XX
XX Example 11; SEQ ID NO 7; 36pp; English.
XX
XX The invention relates to a method of preventing formation or growth of
XX amyloid plaque without causing neurotoxicity which comprises generating a
XX recombinant viral or plasmid vector comprising a DNA sequence encoding at
XX least one amyloid peptide inactivating enzyme operably linked to a
XX promoter. The methods are useful for treating Alzheimer's disease by
XX increasing the activity of an amyloid inactivating enzyme. The present
XX sequence represents the amino acid sequence of a human A beta 1-40
XX insulysin cleavage fragment.
XX
SQ Sequence 21 AA;

Query Match      68.4%; Score 39; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 5 VGSNKGAI 12
|||||

RESULT 34
ADM97747
ID ADM97747 standard; peptide; 21 AA.
XX AC
XX ADM97747;
XX
XX 01-JUL-2004 (first entry)
XX
XX Amyloid beta-derived diffusible ligand peptide #5.
XX
XX immunostimulant; neuroprotective; neurotropic; Alzheimer's disease;
XX Down's syndrome; vaccine; amyloid beta; ADDL;
XX amyloid beta-derived diffusible ligand.
XX
XX Unidentified.
XX
```

```
PN WO2004031400-A2.
XX
PD 15-APR-2004.
XX
PF 01-OCT-2003; 2003WO-US030930.
XX
PR 01-OCT-2002; 2002US-0415074P.
XX
PA (NOUN ) UNIV NORTHWESTERN.
XX
PI Klein W, Krafft GA, Chang L, Gong Y, Viola K, Lambert M;
PI Chromy B, Summa D;
XX
DR WPI; 2004-330196/30.
XX
PT New amyloid beta-derived diffusible ligands, useful in generating an
PT immune response and in preventing, ameliorating or treating Alzheimer's
PT disease, memory and learning deficits, degeneration or malfunction of
PT neurons or Down's syndrome.
XX
XX
PS Claim 36; Page 125; 176pp; English.
XX
CC The present invention relates to a new pharmaceutical composition
CC comprising amyloid beta-derived diffusible ligands (ADDLs) capable of
CC generating an immune response in a host organism, where the composition
CC is a vaccine or a component of a vaccine and where the ADDLs are
CC antigenic, immunogenic or act as a binding molecule when the composition
CC is administered to a host organism. The composition, vaccine or
CC antibodies are useful in inducing an immune response. The composition,
CC peptides, molecules and antibodies are useful in preventing or
CC ameliorating Alzheimer's disease, memory and learning deficits,
CC degeneration or malfunction of neurones and in preventing or treating
CC Down's syndrome. The present sequence is a polypeptide of the invention.
XX
SQ Sequence 21 AA;

Query Match 68.4%; Score 39; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB |||||
2 VGSNKGAI 9

RESULT 35
ADM97746
ID ADM97746 standard; peptide; 21 AA.
XX
AC ADM97746;
XX
DT 01-JUL-2004 (first entry)
XX
DE Amyloid beta-derived diffusible ligand peptide #4.
XX
KW immunostimulant; neuroprotective; nootropic; Alzheimer's disease;
KW Down's syndrome; vaccine; amyloid beta; ADDL;
KW amyloid beta-derived diffusible ligand.
XX
OS Unidentified.
XX
PN WO2004031400-A2.
XX
PD 15-APR-2004.
XX
PF 01-OCT-2003; 2003WO-US030930.
XX
PR 01-OCT-2002; 2002US-0415074P.
XX
PA (NOUN ) UNIV NORTHWESTERN.
XX
PI Klein W, Krafft GA, Chang L, Gong Y, Viola K, Lambert M;
PI Chromy B, Summa D;

WPI; 2004-330196/30.
New amyloid beta-derived diffusible ligands, useful in generating an
immune response and in preventing, ameliorating or treating Alzheimer's
disease, memory and learning deficits, degeneration or malfunction of
neurons or Down's syndrome.
Claim 35; Page 124; 176pp; English.
The present invention relates to a new pharmaceutical composition
comprising amyloid beta-derived diffusible ligands (ADDLs) capable of
generating an immune response in a host organism, where the composition
is a vaccine or a component of a vaccine and where the ADDLs are
antigenic, immunogenic or act as a binding molecule when the composition
is administered to a host organism. The composition, vaccine or
antibodies are useful in inducing an immune response. The composition,
peptides, molecules and antibodies are useful in preventing or
ameliorating Alzheimer's disease, memory and learning deficits,
degeneration or malfunction of neurones and in preventing or treating
Down's syndrome. The present sequence is a polypeptide of the invention.
Sequence 21 AA;

Query Match 68.4%; Score 39; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB |||||
2 VGSNKGAI 9

RESULT 36
ABU63717
ID ABU63717 standard; peptide; 22 AA.
XX
AC ABU63717;
XX
DT 15-OCT-2003 (first entry)
XX
DE Rat amyloid beta 1-40 (Abetal-40) peptide insulysin cleavage product #10.
XX
KW Rat; amyloid beta; Abeta; amyloid fibril; amyloid plaque; neurotoxicity;
KW amyloid peptide-inactivating enzyme; hydrolysis; zinc metalloproteinase;
KW insulin degrading enzyme; IDE; insulysin; neprilysin; peptide therapy;
KW Alzheimer's disease; nootropic; neuroprotective.
XX
OS Rattus sp.
XX
PN US2003083277-A1.
XX
PD 01-MAY-2003.
XX
PF 26-FEB-2001; 2001US-00792079.
XX
PR 24-FEB-2000; 2000US-0184826P.
XX
PA (HERS/) HERSH L B.
XX
PI Hersh LB;
XX
DR WPI; 2003-576623/54.
XX
PT Preventing formation or growth of amyloid fibrils or plaques without
PT causing neurotoxicity, useful for treating Alzheimer's disease, comprises
PT administering an amyloid peptide inactivating enzyme.
XX
PS Example 11; Page 9; 20pp; English.
XX
CC The invention discloses a method for preventing the formation or growth
CC of amyloid fibrils or plaques without causing neurotoxicity. The method
CC comprises administering an inactivation effective amount of an amyloid
```

CC peptide-inactivating enzyme to a mammal. The strategy is to hydrolyse the  
CC amyloid beta (Abeta) peptides before they form amyloid plaques using the  
CC zinc metalloprotease insulin degrading enzyme (IDE), insulin or  
CC neprilysin. The methods and enzymes are useful for treating (e.g peptide  
CC therapy) Alzheimer's disease. The enzymes are useful for inducing the  
CC synthesis of endogenous amyloid inactivating enzymes, such as insulin  
CC or neprilysin, within the brain of the affected individuals. The sequence  
CC presented is a Abeta1-40 peptide insulin cleavage product  
XX  
XX Sequence 22 AA;

Query Match 68.4%; Score 39; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 6 VGSNKGAI 13  
|||||

RESULT 37  
ADF55646  
ID ADF55646 standard; peptide; 22 AA.  
AC ADF55646;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX Human A beta 1-40 insulin cleavage fragment #10.  
DE  
XX  
XX amyloid plaque; neurotoxicity; amyloid peptide inactivating enzyme;  
KW Alzheimer's disease; human; A beta 1-40; insulin.  
XX  
XX Homo sapiens.  
OS  
XX US2003165481-A1.  
PN  
XX  
XX 04-SEP-2003.  
PD  
XX  
XX 03-JUN-2002; 2002US-00159279.  
PF  
XX  
XX 24-FEB-2000; 2000US-0184826P.  
PR  
XX 26-FEB-2001; 2001US-00792079.  
PR  
XX (HERS/) HERSH L B.  
PA  
XX  
XX Herah LB;  
PI  
XX  
XX WPI; 2003-898030/82.  
DR  
XX  
XX Preventing formation or growth of amyloid plaques without causing  
PT neurotoxicity, useful for treating Alzheimer's disease, by generating a  
PT vector comprising a DNA sequence encoding at least one amyloid peptide  
PT inactivating enzyme.  
XX  
XX Example 11; SEQ ID NO 10; 36pp; English.

XX The invention relates to a method of preventing formation or growth of  
CC amyloid plaque without causing neurotoxicity which comprises generating a  
CC recombinant viral or plasmid vector comprising a DNA sequence encoding at  
CC least one amyloid peptide inactivating enzyme operably linked to a  
CC promoter. The methods are useful for treating Alzheimer's disease by  
CC increasing the activity of an amyloid inactivating enzyme. The present  
CC sequence represents the amino acid sequence of a human A beta 1-40  
CC insulin cleavage fragment.  
XX  
XX Sequence 22 AA;

Query Match 68.4%; Score 39; DB 7; Length 22;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9

DB 6 VGSNKGAI 13  
|||||

RESULT 38  
AAB91832  
ID AAB91832 standard; peptide; 24 AA.  
XX  
XX AAB91832;  
AC  
XX  
XX 22-JUN-2001 (first entry)  
XX  
XX Amyloid beta-protein fragment peptide SEQ ID NO:1008.  
DE  
XX  
XX Protection; endogenous therapeutic peptide; peptide; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX WO200069900-A2.  
PN  
XX  
XX 23-NOV-2000.  
PD  
XX  
XX 17-MAY-2000; 2000WO-US013576.  
PF  
XX  
XX 17-MAY-1999; 99US-0134406P.  
PR  
XX 10-SEP-1999; 99US-0153406P.  
PR  
XX 15-OCT-1999; 99US-0159783P.  
PR  
XX (CONJ-) CONJUCHEM INC.  
PA  
XX  
XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
XX  
XX WPI; 2001-112059/12.  
DR  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptide degradation, useful for increasing length of in vivo activity.  
PT  
XX  
XX Disclosure; Page 525; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention  
XX  
XX Sequence 24 AA;

Query Match 68.4%; Score 39; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9  
DB 8 VGSNKGAI 15  
|||||

RESULT 39  
AAB91805

DE AAB91805 standard; peptide; 24 AA.  
XX AAB91805;  
AC  
XX 22-JUN-2001 (first entry)  
DT  
XX  
DE Amyloid beta-protein fragment peptide SEQ ID NO:981.  
XX  
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS  
XX WO200069900-A2.  
XX  
XX 23-NOV-2000.  
XX  
XX 17-MAY-2000; 2000WO-US013576.  
XX  
XX 17-MAY-1999; 99US-0134406P.  
XX  
XX 10-SEP-1999; 99US-0153406P.  
XX  
XX 15-OCT-1999; 99US-0159783P.  
XX  
XX (CONJ-) CONJUCHEM INC.  
XX  
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
XX  
XX WPI; 2001-112059/12.  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
XX peptidase degradation, useful for increasing length of in vivo activity.  
XX  
XX Disclosure; Page 515; 733pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)  
XX comprising a therapeutically active amino acid region (III) and a  
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
XX a less therapeutically active amino acid region (IV), which covalently  
XX bonds with amino/hydroxyl/thiol groups on blood components to form a  
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
XX factors and neurotransmitters, to protect them from peptidase activity in  
XX vivo for the treatment of various disorders. Endogenous therapeutic  
XX peptides are not suitable as drug candidates as they require frequent  
XX administration due to rapid degradation by peptidases in the body.  
XX Modifying and attaching therapeutic peptides to albumin prevents or  
XX reduces the action of peptidases to increase length of activity (half  
XX life) and specificity as bonding to large molecules decreases  
XX intracellular uptake and interference with physiological processes.  
XX AAB90829 to AAB92441 represent peptides which can be used in the  
XX exemplification of the present invention  
XX  
SQ Sequence 24 AA;  
Query Match 68.4%; Score 39; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db |||||  
8 VGSNKGAI 15  
RESULT 40  
AEB09195  
ID AEB09195 standard; peptide; 24 AA.  
XX  
XX AEB09195;  
AC  
XX 25-AUG-2005 (first entry)  
DT  
XX

DE Human beta-amyloid (Abeta) peptide, SEQ ID 6.  
XX  
XX Alzheimers disease; beta-amyloid; probe.  
XX  
OS Homo sapiens.  
XX  
XX WO2005057166-A2.  
XX  
XX 23-JUN-2005.  
XX  
XX 03-DEC-2004; 2004WO-US040309.  
XX  
XX 04-DEC-2003; 2003US-00728246.  
XX  
XX (ARET-) ARETE ASSOC.  
XX  
XX Orser C, Grosset A, Davidson E;  
XX  
XX WPI; 2005-435644/44.  
XX  
XX Detection of conformationally altered proteins or prions in sample useful  
XX for diagnosing e.g. Alzheimer's disease involves reacting the sample with  
XX palindromic probe having amino acid sequence of specific protein.  
XX  
XX Claim 17; SEQ ID NO 6; 71pp; English.  
XX  
XX The present invention relates to a method for detecting betabeta-sheet  
XX conformation (C1) of insoluble proteins or prions in a sample. The method  
XX involves reacting the sample with at least one alpha-helix or random coil  
XX conformational probe (P1) that interacts with (C1) to undergo a  
XX conformational conversion to a predominantly betabeta-sheet conformation  
XX and form detectable aggregates with (C1); and detecting levels of  
XX aggregates. The levels of aggregates correlate to levels of (C1). (P1) is  
XX preferably a palindromic peptide probe which produces betabeta sheets when  
XX complexed with the target protein. The method is useful for diagnosing a  
XX disease associated with conformationally altered proteins or prions (such  
XX as low-density lipoprotein receptor, cystic fibrosis transmembrane  
XX regulator, Huntingtin, Abeta peptide, prion, insulin-related amyloid,  
XX hemoglobin, a synuclein, rhodopsin, crystalline and p53) e.g. Alzheimer's  
XX disease, prion disease, Creutzfeldt Jakob disease, scrapie and bovine  
XX spongiform encephalopathy (PrP(sc)), amyotrophic lateral sclerosis (SOD  
XX or neurofilament), Pick's disease, Parkinson's disease, Frontotemporal  
XX dementia, type II diabetes, multiple myeloma-plasma cell dyscrasias,  
XX familial amyloidotic polyneuropathy, medullary carcinoma of thyroid,  
XX chronic renal failure, congestive heart failure, senile cardiac and  
XX systemic amyloidosis (transhyretin), chronic inflammation,  
XX atherosclerosis, familial amyloidosis or Huntington's disease. The  
XX present sequence was used to illustrate the invention.  
XX  
SQ Sequence 24 AA;  
Query Match 68.4%; Score 39; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VGSNKGAI 9  
Db |||||  
14 VGSNKGAI 21  
Search completed: January 28, 2006, 00:57:23  
Job time : 82 secs

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